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OM protein - protein search, using sw model

Run on: October 8, 2002, 10:15:15 ; Search time 51.43 Seconds
(without alignments)
339.074 Million cell updates/sec

Title: SEQ6THRAT73

Perfect score: 816

Sequence: 1 YFKLESKSLVIRNLNDQVL.....LKKEDELGDRSIMFTVQNE 157

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 11107396 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

A_Geneseq_032802.*

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19: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.*
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21: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	816	100.0	157	19	AAW77077 Human interleukin
2	816	100.0	157	21	AAI57570 Human interleukin
3	816	100.0	157	22	AAE06661 Human interleukin
4	816	100.0	157	22	AAE65294 Human interleukin
5	816	100.0	157	22	AAE65351 Human interleukin
6	816	100.0	157	21	AAE85167 Human interleukin
7	816	100.0	180	19	AAW48959 Wild-type human in
8	816	100.0	193	18	AAW22047 Interferon gamma 1
9	816	100.0	193	19	AAW46592 Amino acid sequenc
10	816	100.0	193	22	AAE30541 A human IL-18 with
11	816	100.0	193	22	AAE63830 Amino acid sequenc

12	813	99.6	193	19	AAW77082 Interleukin 18 act
13	811	99.4	157	17	AAR99564 Human interferon-g
14	811	99.4	157	17	AAR99558 Human mature inter
15	811	99.4	157	18	AAW15701 Interferon-gamma 1
16	811	99.4	157	18	AAW24258 Human protein for
17	811	99.4	157	19	AAW77158 Human interleukin-
18	811	99.4	157	19	AAW63810 IFN-gamma inducing
19	811	99.4	157	19	AAW37741 Interleukin-18 rec
20	811	99.4	157	19	AAW52176 Interleukin-gamma 1
21	811	99.4	157	20	AAI39799 Human interleukin-
22	811	99.4	157	21	AAI44597 Sequence of a matu
23	811	99.4	157	21	AAI53904 Human interleukin-
24	811	99.4	157	22	AAE82408 Human interferon-g
25	811	99.4	193	17	AAR99560 Interferon-gamma 1
26	811	99.4	193	19	AAW37740 Interferon-gamma 1
27	811	99.4	193	19	AAW52172 Interferon-gamma p
28	811	99.4	193	19	AAW47429 Amino acid sequenc
29	811	99.4	193	21	AAI53908 Human interleukin-
30	811	99.4	193	22	AAE82409 Interferon gamma 1
31	808	99.0	193	18	AAW31757 Human interleukin
32	806	98.8	157	19	AAW77083 Mutant human inter
33	806	98.8	157	19	AAW48961 Human interleukin
34	806	98.8	181	21	AAE23797 Human interleukin
35	797	97.7	193	22	AAI72608 Macaca cynomolgus
36	796	97.5	157	19	AAW77084 Human interleukin
37	796	97.5	157	19	AAW77085 Human interleukin
38	796	97.5	157	19	AAW48962 Mutant human inter
39	796	97.5	157	19	AAW48963 Mutant human inter
40	787	96.4	157	19	AAW77080 Human interleukin
41	787	96.4	157	19	AAW77088 Human interleukin
42	787	96.4	157	19	AAW48966 Mutant human inter
43	786	96.3	157	19	AAW77086 Human interleukin
44	786	96.3	157	19	AAW48964 Mutant human inter
45	777	95.2	157	19	AAW77081 Human interleukin

ALIGNMENTS

RESULT 1

AAW77077
ID AAW77077 standard; peptide; 157 AA.
XX AC AAW77077;
XX AC
XX AC
DT 16-NOV-1998 (first entry)
XX Human interleukin 18.
DE Human interleukin-18; IL-18; osteoclast; hypercalcaemia; osteopenia;
KW Human; osteoclastoma Behcet's syndrome; osteosarcoma; arthropathy; osteoporosis;
KW chronic rheumatoid arthritis; deformity ostitis; primary hyperthyroidism.
XX Homo sapiens.
XX EP861663-A2.
XX
XX
PD 02-SEP-1998.
PF 24-FEB-1998; 98EP-0301352.
XX
PR 25-FEB-1997; 97JP-0055468.
XX
XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
XX Gillespie MT, Horwood NJ, Kurimoto M, Udagawa N;
XX WPI: 1998-448964/39.
XX N-PSDB; AAV48226.

Use of interleukin-18 to inhibit osteoclast formation - in treatment of e.g. hypercalcaemia, osteoclastoma, Behcet's syndrome, osteosarcoma, chronic rheumatoid arthritis, deformity ostitis, PT

PT primary hyperthyroidism and osteoporosis
XX
PS Claim 4; Page 18; 56pp; English.
XX
CC Interleukin-18 (IL-18) or a functional equivalent can be used for
CC inhibition of osteoclast formation. IL-18 is used for treating or
CC preventing osteoclast-related diseases e.g. hypercalcaemia, osteoclastoma
CC Behcet's syndrome, osteosarcoma, arthropathy, chronic rheumatoid
CC arthritis, deformity ostitis, primary hyperthyroidism, osteopenia and
CC osteoporosis.
XX
SQ Sequence 157 AA;

Query Match 100.0%; Score 816; DB 19; Length 157;
Best Local Similarity 100.0%; Pred. No. 1.2e-83;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSCDRNAPRTIFIISMYKDSQPRGM 60
DB 1 yfgklesklsvirnlndqvlfidggnrplfedmtdsdcdrnaprtifiismykdsqprgm 60
QY 61 AVTISVCKEISTLSCENKIISFKEMPPDNKDKSDIIFQSRVPGCHDNKMQFESSY 120
DB 61 avtisvckekistlscenkiiisfkemppdnkdkdsdiiiffqsrvgpghdnkmgfessy 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
DB 121 egyflacekerdlfklllkkedelgdrsimftvqned 157

RESULT 2
AAV57570
ID AAV57570 standard; protein; 157 AA.
XX
AC AAV57570;
XX
DT 06-MAR-2000 (first entry)
XX
DE Human interleukin 18 protein sequence SEQ ID NO:1.
XX
KW Human; Interleukin 18; IL-18; potentiator; IGIF; tumour; cancer;
KW Interferon-gamma-inducing factor; growth inhibition; cytostatic.
XX
OS Homo sapiens.
XX
PN WO959565-A1.
XX
PD 25-NOV-1999.
XX
PF 20-MAY-1999; 99WO-US11160.
XX
PR 21-MAY-1998; 98US-0086560.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI Johnson RK;
XX
WPI; 2000-062368/05.
XX
PT New polypeptides, useful for preparation of composition for preventing
PT and/or treating cancer by inhibiting tumor growth -
XX
XX
PS Claim 1; Page 49-50; 53pp; English.

CC The present sequence represents human interleukin 18 (IL-18). The
CC present invention describes a compound comprising human or murine IL-18
CC in combination with a chemotherapeutic agent (I). Also described are:
CC (1) a method of preventing and/or treating cancer in a mammal comprising
CC the administration of a cancer inhibiting amount of (I) comprising the
CC IL-18 protein and the chemotherapeutic agent and optionally a
CC pharmaceutically acceptable carrier; and (2) a method of inhibiting the
CC growth of tumour cells in a mammal sensitive to a composition comprising

CC human IL-18 and/or murine IL-18 and the chemotherapeutic agent (and
CC optionally a pharmaceutically acceptable carrier), comprising
CC administering to a mammal afflicted with the tumour cells an effective
CC tumour cell growth inhibiting amount of (I). The IL-18 protein in
CC conjunction with a chemotherapeutic agent is useful in a method for
CC preventing and/or treating cancer in mammals by inhibiting the growth
CC of tumours or cancerous cells in mammals.
XX
SQ Sequence 157 AA;

Query Match 100.0%; Score 816; DB 21; Length 157;
Best Local Similarity 100.0%; Pred. No. 1.2e-83;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSCDRNAPRTIFIISMYKDSQPRGM 60
DB 1 yfgklesklsvirnlndqvlfidggnrplfedmtdsdcdrnaprtifiismykdsqprgm 60
QY 61 AVTISVCKEISTLSCENKIISFKEMPPDNKDKSDIIFQSRVPGCHDNKMQFESSY 120
DB 61 avtisvckekistlscenkiiisfkemppdnkdkdsdiiiffqsrvgpghdnkmgfessy 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
DB 121 egyflacekerdlfklllkkedelgdrsimftvqned 157

RESULT 3
AAE06661
ID AAE06661 standard; protein; 157 AA.
XX
AC AAE06661;
XX
DT 16-OCT-2001 (first entry)
XX
DE Human interleukin-1gamma (IL-1gamma) protein.
XX
KW Human; Interleukin-1gamma; IL-1gamma; virucide; hepatotropic; fever;
KW immunological disorder; tumour; inflammatory disorder; hypoglycaemia;
KW autoimmune disease; pulmonary tuberculosis; fulminant hepatitis; leprosy;
KW psoriasis; viral infection; allergy; cytokine; HIV; drug screening.
XX
OS Homo sapiens.
XX
PN WO200157219-A2.
XX
PD 09-AUG-2001.
XX
PF 01-FEB-2001; 2001WO-US03285.
XX
PR 02-FEB-2000; 2000US-0179638.
XX
PA (SCHE) SCHERING CORP.
XX
PI Debets JEMA, Timans JC, Bazan JF, Kastelein RA;
XX
WPI; 2001-488886/53.
XX
PT Novel isolated or recombinant antigenic interleukin-1 delta or epsilon
PT polypeptide useful for treating conditions exhibiting abnormal
PT expression of interleukin such as immunological disorders, tumor and
PT allergy -
XX
PS Disclosure; Fig 1; 103pp; English.
XX
CC The invention relates to recombinant antigenic Interleukin-1 like
CC molecules and their corresponding nucleic acid sequences, designated
CC as interleukin-1delta (IL-1delta) and interleukin-1epsilon (IL-1epsilon).
CC IL-1delta and IL-1epsilon are useful for treating conditions exhibiting
CC abnormal expression of the interleukin such as immunological disorders,
CC tumours, inflammatory disorders, fever, hypoglycaemia, psoriasis,
CC allergy, autoimmune diseases and infectious diseases (e.g., pulmonary

CC tuberculosis, leprosy, fulminant hepatitis, and viral infections such as
 CC HIV). The invention also relates to methods of using the composition
 CC containing IL-delta or IL-lepsilon for both diagnostic and therapeutic
 CC utilities. IL-delta is used as an immunogen for the production of
 CC antisera or antibodies specific, e.g., capable of distinguishing between
 CC IL-1 family members and an IL-delta, for the interleukin or its
 CC fragment. The purified interleukin is used as a reagent to detect any
 CC antibodies generated in response to the presence of elevated levels of
 CC expression, or immunological disorders which lead to antibody production
 CC to the endogenous cytokine. The invention also contemplates the use of
 CC competitive drug screening assays. The present sequence is human
 CC interleukin-1gamma (IL-1gamma) protein related to the invention.
 XX
 SQ Sequence 157 AA;

Query Match 100.0%; Score 816; DB 22; Length 157;
 Best Local Similarity 100.0%; Pred. No. 1.2e-83;
 Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSCDRNAPRTIPIISMVKDSQPRGM 60
 DB 1 yfgklesklsvirnlndqvlfidqgnrplfedmtdsdcdrnaprtifiismykdspgrgm 60
 QY 61 AVTISVKCEKISTLSCEKNIISFKEMNPPDNIKDKSDIIFFORSVPGHDKMKQFESSY 120
 DB 61 avtisvkceki stlscekn iisfkemppdn iktksdi iffor svpg hdkmkqfessy 120
 QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
 DB 121 egyflacekerdlfklllkkedelgdrsimftvqned 157

RESULT 4
 AAG65294
 ID AAG65294 standard; protein; 157 AA.
 XX AAG65294;
 XX
 DT 30-NOV-2001 (first entry)
 XX
 DE Human interleukin-18 (IL-18) protein fragment.
 XX
 KW IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;
 KW nootropic; neurological; antiinflammatory; antiparkinsonian; cardiant;
 KW immunosuppressive; antidepressant; neuroleptic; hepatotropic.
 XX
 OS Homo sapiens.
 XX
 PN WO200158956-A2.
 XX
 PD 16-AUG-2001.
 XX
 XX 09-FEB-2001; 2001WO-US04170.
 XX
 XX 10-FEB-2000; 2000US-0181608.
 XX
 PA (BADI) BASF AG.
 XX
 PI Ghayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfeld J;
 PI Duncan AR, Brocklehurst SM, Mankovich J, Shorrocks CP, Thompson JB;
 PI Lennard SN;
 DR WPI; 2001-550020/61.
 XX
 PT Novel antibodies and compounds capable of binding to human
 PT interleukin-18 useful for treating, e.g., inflammatory disorders,
 PT neurological disorders, heart failure, myocardial infarction, and
 PT autoimmune diseases -
 XX
 PS Disclosure; Page 9; 91pp; English.
 XX
 CC The invention provides isolated antibodies, or antigen-binding portions,

CC that are capable of binding to human interleukin-18 (IL-18). The
 CC antibodies may be used to inhibit human IL-18 activity in, and treat a
 CC disorder where IL-18 is detrimental in, a human subject suffering from,
 CC inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,
 CC inflammatory bowel disease, and osteoarthritis), neurological disorders
 CC (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and
 CC stroke), heart failure, myocardial infarction, autoimmune diseases such
 CC as autoimmune hepatitis and autoimmune neutropenia, and mental disorders
 CC (e.g., depression and schizophrenia). Treatment with an anti-IL-18
 CC antibody may occur before, concurrent, or after administration of a
 CC second agent selected from an antibody, or fragment, capable of binding
 CC human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,
 CC cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory
 CC agents. The present sequence represents a human IL-18 protein fragment.
 XX
 SQ Sequence 157 AA;

Query Match 100.0%; Score 816; DB 22; Length 157;
 Best Local Similarity 100.0%; Pred. No. 1.2e-83;
 Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0
 QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSCDRNAPRTIPIISMVKDSQPRGM 60
 DB 1 yfgklesklsvirnlndqvlfidqgnrplfedmtdsdcdrnaprtifiismykdspgrgm 60
 QY 61 AVTISVKCEKISTLSCEKNIISFKEMNPPDNIKDKSDIIFFORSVPGHDKMKQFESSY 120
 DB 61 avtisvkceki stlscekn iisfkemppdn iktksdi iffor svpg hdkmkqfessy 120
 QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
 DB 121 egyflacekerdlfklllkkedelgdrsimftvqned 157

RESULT 5
 AAG65351
 ID AAG65351 standard; protein; 157 AA.
 XX AAG65351;
 XX
 DT 30-NOV-2001 (first entry)
 XX
 DE Human interleukin-18 (IL-18) protein fragment.
 XX
 KW IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;
 KW nootropic; neurological; antiinflammatory; antiparkinsonian; cardiant;
 KW immunosuppressive; antidepressant; neuroleptic; hepatotropic.
 XX
 OS Homo sapiens.
 XX
 PN WO200158956-A2.
 XX
 PD 16-AUG-2001.
 XX
 XX 09-FEB-2001; 2001WO-US04170.
 XX
 XX 10-FEB-2000; 2000US-0181608.
 XX
 PA (BADI) BASF AG.
 XX
 PI Ghayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfeld J;
 PI Duncan AR, Brocklehurst SM, Mankovich J, Shorrocks CP, Thompson JB;
 PI Lennard SN;
 DR WPI; 2001-550020/61.
 XX
 PT Novel antibodies and compounds capable of binding to human
 PT interleukin-18 useful for treating, e.g., inflammatory disorders,
 PT neurological disorders, heart failure, myocardial infarction, and
 PT autoimmune diseases -
 XX
 PS Disclosure; Page 14; 91pp; English.

XX The invention provides isolated antibodies, or antigen-binding portions,
 CC that are capable of binding to human interleukin-18 (IL-18). The
 CC antibodies may be used to inhibit human IL-18 activity in, and treat a
 CC disorder where IL-18 is detrimental in, a human subject suffering from,
 CC inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,
 CC inflammatory bowel disease, and osteoarthritis), neurological disorders
 CC (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and
 CC stroke), heart failure, myocardial infarction, autoimmune diseases such
 CC as autoimmune hepatitis and autoimmune neutropenia, and mental disorders
 CC (e.g., depression and schizophrenia). Treatment with an anti-IL-18
 CC antibody may occur before, concurrent, or after administration of a
 CC second agent selected from an antibody, or fragment, capable of binding
 CC human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,
 CC cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory
 CC agents. The present sequence represents a human IL-18 protein fragment.
 XX Sequence 157 AA;

Query Match 100.0%; Score 816; DB 22; Length 157;
 Best Local Similarity 100.0%; Pred. No. 1.2e-83;
 Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNNDQVLFIDQGNRPFLFEDMTSDCRDNPRTFIISMYKDSQPRGM 60
 Db 1 yfgklesklsvirnndqvlfidqgnrplfedmtsdcrdnprtfiismykdsqprgm 60
 QY 61 AVTISVKCEKISTLSCENKIISFKEMNPPDNKDKTSIIFFQRSVPGHDNKMQFESSY 120
 Db 61 avtisvkcekistlscenkliisfkemppdnikdtktsdiiffqrsvpgghdnkmqfessy 120
 QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
 Db 121 egyflacekerdlfklikkedelgdrsimftvqned 157

RESULT 6
 AAY85167
 ID AAY85167 standard; Protein; 158 AA.
 XX AAY85167;
 XX 23-JUN-2000 (first entry)
 DE Human interleukin-18 (IL-18) amino acid sequence.
 XX Interleukin-18; production; IL-18; human; medical injection product.
 KW Homo sapiens.
 OS CN1243130-A.
 PN 02-FEB-2000.
 PD 24-JUL-1998; 98CN-0103307.
 PF 24-JUL-1998; 98CN-0103307.
 PR (WUGG/) WU G.
 XX Wu G, Liu Z;
 PI WPI; 2000-340020/30.
 DR N-PSDB; AAA10526.

XX Preparation method for engineering bacteria for recombination of human
 CC interleukin-18 and its product thereof -
 PS Claim 1; Page 2; 17pp; English.
 XX This sequence represents the human interleukin-18 (IL-18) amino acid
 CC sequence. The invention relates to a method for engineering bacterium for

CC recombination of human IL-18 and a method for the preparation of IL-18. A
 CC primer containing a restriction endonuclease site can be used to
 CC accurately obtain the IL-18 gene containing 474 nucleotides, and uses the
 CC stop codon preferred by coli bacillus to raise the expression rate. The
 CC method uses a high-amplification culture medium to increase the
 CC expression level and only requires a one-step purification process to
 CC obtain a medical injection-pure product.
 XX Sequence 158 AA;

Query Match 100.0%; Score 816; DB 21; Length 158;
 Best Local Similarity 100.0%; Pred. No. 1.2e-83;
 Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNNDQVLFIDQGNRPFLFEDMTSDCRDNPRTFIISMYKDSQPRGM 60
 Db 1 yfgklesklsvirnndqvlfidqgnrplfedmtsdcrdnprtfiismykdsqprgm 61
 QY 61 AVTISVKCEKISTLSCENKIISFKEMNPPDNKDKTSIIFFQRSVPGHDNKMQFESSY 120
 Db 62 avtisvkcekistlscenkliisfkemppdnikdtktsdiiffqrsvpgghdnkmqfessy 121
 QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
 Db 122 egyflacekerdlfklikkedelgdrsimftvqned 158

RESULT 7
 AAW48959
 ID AAW48959 standard; Peptide; 180 AA.
 XX AAW48959;
 XX 25-SEP-1998 (first entry)
 DE Wild-type human interferon-gamma inducing factor.
 KW Interferon-gamma inducing factor; interferon-gamma; killer cell;
 KW antitumour agent; antiviral agent; antimicrobial agent; tumour; IGIF;
 KW hepatitis; malaria; tuberculosis; renal carcinoma; rheumatism; AIDS;
 KW osteoporosis; thrombopenia; acquired immunodeficiency syndrome.
 OS Homo sapiens.
 EH Key Location/Qualifiers
 FT Peptide 1..23 /note= "Signal peptide"
 FT Protein 24..180 /note= "Mature human IGIF which is claimed by the
 FT inventors under claim 3 in the specification"

XX EP845530-A2.
 PN 03-JUN-1998.
 PD 28-NOV-1997; 97EP-0309632.
 PF 14-NOV-1997; 97JP-0329715.
 PR 29-NOV-1996; 96JP-0333037.
 PR 21-JAN-1997; 97JP-0020906.
 XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 XX Kurimoto M, Okamoto I, Yamamoto K;
 PI WPI; 1998-288747/26.
 DR N-PSDB; AAV32754.

XX Mutants of interferon-gamma inducing polypeptide - useful as
 CC antitumour, antiviral, antimicrobial or anti-immunopathic agents
 PS Claim 3; pages 36-37; 59pp; English.

```
XX The present sequence represents the wild-type human interferon-gamma
CC inducing factor (IGIF). The invention provides for mutant human and
CC mouse interferon-gamma inducing factors in which one or more cysteine
CC residues are replaced with different residues at or away from the
CC consensus sequences shown in AAW48956-W48958. The mutant IGIFs are
CC capable of stimulating immunocompetent cells for the production of
CC interferon-gamma and are claimed to be less toxic, more active and
CC stable than the corresponding wild type IGIF. The mutant IGIFs are also
CC claimed to enhance killer cell cytotoxicity and/or induce killer cell
CC formation, and may therefore be useful as antitumour agents, antitumour
CC immunotherapeutics, antiviral agents and antimicrobial agents. The
CC mutant IGIFs are also claimed to be useful for treating hepatitis,
CC acquired immunodeficiency syndrome (AIDS), malaria, tuberculosis, solid
CC malignant tumours (e.g. renal carcinoma), rheumatism, osteoporosis and
CC thrombopenia caused by radiation- and chemo-therapy.
XX
SQ Sequence 180 AA;
Query Match 100.0%; Score 816; DB 19; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.5e-83;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYSKDSQPRGM 60
Db 24 yfgklesklsvirnlndqvlfdqgnrplfedmtsdcrdnprtifiismyskdsqprgm 83
Qy 61 AVTISVKCEKISTLSCENKIISFKEMNPPDNIKDTKSDIIFQRSVPGHDNKMQFESSY 120
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Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
Db 144 egyflacekerdlfklllkkeedelgdrsimftvqned 180
RESULT 8
AAW22047
ID AAW22047 standard; Protein; 193 AA.
XX
AC AAW22047;
XX
DT 14-JAN-1998 (first entry)
XX
DE Interferon gamma inducing factor-2 (IGIF-2) protein.
XX
KW Interferon gamma inducing factor-2; IGIF-2; leucocyte; lymphocyte;
KW inflammation; proliferation; differentiation; maturation; tissue damage;
KW human.
XX
OS Homo sapiens.
XX
PN W09724441-A1.
XX
PD 10-JUL-1997.
XX
PF 20-DEC-1996; 96WO-US20432.
XX
PR 29-DEC-1995; 95US-0580667.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Cocks BG, Coleman R, Hawkins PR;
XX
DR WPI; 1997-363677/33.
DR N-PSDB; AAT74987.
XX
XX Novel interferon gamma inducing factor-2 - used to screen for
PT compounds to diagnose, treat or prevent tissue damage associated
PT with inflammation
XX
PS Claim 1; Page 46; 60pp; English.
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```
XX This is the protein sequence of interferon gamma inducing factor-2
CC (IGIF-2). An IGIF-2 variant (AAW31757) and an IGIF variant (AAW22049),
CC which may be an alternate transcript, also exist. Probes derived from
CC the nucleic acid sequences can be used to quantify the expression of
CC IGIF-2 in conditions that are associated with inflammation or aberrant
CC expression of IGIF-2. The protein can be used to screen for compounds
CC that interact with IGIF-2, such as antibodies, antagonists or other
CC inhibitors (especially ribozymes or antisense sequences) of IGIF-2
CC expression or activity. The protein can also be used to diagnose,
CC prevent or treat IGIF-2 induction of proliferation, differentiation or
CC maturation of leucocytes or lymphocytes, especially in relation to tissue
CC damage associated with inflammation.
XX
SQ Sequence 193 AA;
Query Match 100.0%; Score 816; DB 18; Length 193;
Best Local Similarity 100.0%; Pred. No. 1.6e-83;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYSKDSQPRGM 60
Db 37 yfgklesklsvirnlndqvlfdqgnrplfedmtsdcrdnprtifiismyskdsqprgm 96
Qy 61 AVTISVKCEKISTLSCENKIISFKEMNPPDNIKDTKSDIIFQRSVPGHDNKMQFESSY 120
Db 97 avtisvckeekistlscenkiisfkemnpddnikdtksdilffqrsvpghdnkmqfessy 156
Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
Db 157 egyflacekerdlfklllkkeedelgdrsimftvqned 193
RESULT 9
AAW46592
ID AAW46592 standard; Protein; 193 AA.
XX
AC AAW46592;
XX
DT 21-MAY-1998 (first entry)
XX
DE Amino acid sequence of human interleukin-1-gamma.
XX
KW Interleukin-1-gamma; IL-1-gamma; mouse; cytokine; IGIF; interferon-gamma;
KW induction; antibody; diagnostic assay; fusion protein; activity;
KW immunological disorder; allergy.
XX
OS Homo sapiens.
XX
PH Key Location/Qualifiers
FT Region 41..47 "beta-1 region"
FT Region 55..59 "beta-2 region"
FT Region 64..68 "beta-3 region"
FT Region 83..88 "beta-4 region"
FT Region 96..102 "beta-5 region"
FT Region 108..113 "beta-6 region"
FT Region 115..120 "beta-7 region"
FT Region 137..143 "beta-8 region"
FT Region 147..153 "beta-9 region"
FT Region 160..164 "beta-10 region"
FT Region 170..175 "beta-11 region"
```

```

FH Key      Location/Qualifiers
FT Cleavage-site 33..36
XX          /note= "caspase-8 cleavage site"
XX WO200061768-A2.
XX
XX 19-OCT-2000.
XX
XX 13-APR-2000; 2000WO-IL00220.
XX
XX 13-APR-1999; 99IL-0129427.
XX
XX (YEDA ) YEDA RES & DEV CO LTD.
XX
XX Rubinstein M, Liu B, Novick D, Dinarello C, Graber P;
XX
XX WPI: 2001-006910/01.
XX
XX N-PSDB; AAC62200.
XX
XX Preparation of biologically active molecules from its inactive
XX precursors, comprises mutating their native cleavage site to a site
XX capable of being cleaved by protease and cleaving the mutated molecule
XX
XX Disclosure; Fig 8a-b; 40pp; English.
XX
XX The present sequence represents a human pro interleukin-18 (IL-18)
XX with a caspase-8 cleavage site. The natural cleavage site of IL-18
XX was mutated to a site susceptible to cleavage by a common protease.
XX The specification describes a method for the preparation of biologically
XX active molecules from their biologically inactive precursors. The method
XX comprises mutating the native cleavage site to a site capable of being
XX cleaved by a protease and cleaving the mutated molecule to yield the
XX active compound. The method is especially used to produce active
XX cytokines, such as IL-18.
XX
XX Sequence 193 AA;

Query Match      100.0%; Score 816; DB 19; Length 193;
Best Local Similarity 100.0%; Pred. No. 1.6e-83;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
   |||||||
Db 37 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 96
   |||||||
QY 61 AVTISVKCEKISTLSCENKIISFKENPPDNINKDTKSDIIFFORSVPGHDNKNMQFESSY 120
   |||||||
Db 97 AVTISVKCEKISTLSCENKIISFKENPPDNINKDTKSDIIFFORSVPGHDNKNMQFESSY 156
   |||||||
QY 121 EGYFLACEKERDLFKLILKKEDELGRSMTFTVQNEED 157
   |||||||
Db 157 EGYFLACEKERDLFKLILKKEDELGRSMTFTVQNEED 193
   |||||||

RESULT 10
AAB30541
ID AAB30541 standard; Protein; 193 AA.
XX
XX AAB30541;
XX
XX 06-MAR-2001 (first entry)
XX
XX A human IL-18 with a caspase-8 cleavage site.
XX
XX Protease cleavage site; caspase-1; interleukin-18; IL-18; protease.
XX
XX Synthetic.
XX
XX Homo sapiens.
XX

```

```

FH Key      Location/Qualifiers
FT Cleavage-site 33..36
XX          /note= "caspase-8 cleavage site"
XX WO200061768-A2.
XX
XX 19-OCT-2000.
XX
XX 13-APR-2000; 2000WO-IL00220.
XX
XX 13-APR-1999; 99IL-0129427.
XX
XX (YEDA ) YEDA RES & DEV CO LTD.
XX
XX Rubinstein M, Liu B, Novick D, Dinarello C, Graber P;
XX
XX WPI: 2001-006910/01.
XX
XX N-PSDB; AAC62200.
XX
XX Preparation of biologically active molecules from its inactive
XX precursors, comprises mutating their native cleavage site to a site
XX capable of being cleaved by protease and cleaving the mutated molecule
XX
XX Disclosure; Fig 8a-b; 40pp; English.
XX
XX The present sequence represents a human pro interleukin-18 (IL-18)
XX with a caspase-8 cleavage site. The natural cleavage site of IL-18
XX was mutated to a site susceptible to cleavage by a common protease.
XX The specification describes a method for the preparation of biologically
XX active molecules from their biologically inactive precursors. The method
XX comprises mutating the native cleavage site to a site capable of being
XX cleaved by a protease and cleaving the mutated molecule to yield the
XX active compound. The method is especially used to produce active
XX cytokines, such as IL-18.
XX
XX Sequence 193 AA;

Query Match      100.0%; Score 816; DB 22; Length 193;
Best Local Similarity 100.0%; Pred. No. 1.6e-83;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
   |||||||
Db 37 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 96
   |||||||
QY 61 AVTISVKCEKISTLSCENKIISFKENPPDNINKDTKSDIIFFORSVPGHDNKNMQFESSY 120
   |||||||
Db 97 AVTISVKCEKISTLSCENKIISFKENPPDNINKDTKSDIIFFORSVPGHDNKNMQFESSY 156
   |||||||
QY 121 EGYFLACEKERDLFKLILKKEDELGRSMTFTVQNEED 157
   |||||||
Db 157 EGYFLACEKERDLFKLILKKEDELGRSMTFTVQNEED 193
   |||||||

RESULT 11
AAG63830
ID AAG63830 standard; Protein; 193 AA.
XX
XX AAG63830;
XX
XX 26-NOV-2001 (first entry)
XX
XX Amino acid sequence of human interleukin 18 (IL-18).
XX
XX T-cell-helper type 2 response; Th2 response; T cell mediated response;
XX allergic response; interleukin 18; IL-18; IGE-mediated allergy;
XX allergic asthma; anaphylactic reaction; asthma associated allergy;
XX IGE dependent allergic rhinoconjunctivitis.
XX
XX Homo sapiens.
XX

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```
PN W0200168896-A1.
XX
PD 20-SEP-2001.
XX
PF 02-MAR-2001; 2001WO-US06869.
XX
PR 10-MAR-2000; 2000US-0188311.
XX
PA (STRD ) UNIV LELAND STANFORD JUNIOR.
XX
PI Levy S, Dekruyff RH, Umetsu DT, Maecker H;
XX WPI; 2001-570874/64.
XX DR N-PSDB; AAH78060.
XX
PT Reducing antigen specific immune response in conditions such as asthma,
PT allergic rhinitis, by reducing a T-cell-helper type 2 T cell mediated
PT antigen-specific allergic response .
XX
PS Disclosure; Page 36; 38pp; English.
XX
CC The specification describes a method for reducing a T-cell-helper
CC type 2 (Th2) T cell mediated antigen-specific allergic response. The
CC method comprises administering a DNA construct encoding a fusion
CC protein of interleukin 18 (IL-18) and an antigen associated with the
CC allergic response. The method is useful for reducing a Th2 T cell
CC mediated antigen-specific allergic response especially IgE-mediated
CC allergic asthma or anaphylactic reactions or IgE dependent allergic
CC rhinoconjunctivitis, and for treating asthma associated allergies where
CC the allergies are ongoing at the time of the administration. The
CC present sequence represents a human IL-18, and is used to construct
CC fusion proteins of the invention.
XX
SQ Sequence 193 AA;

Query Match 100.0%; Score 816; DB 22; Length 193;
Best Local Similarity 100.0%; Pred. No. 1.6e-83;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTFIISMYKDSQPRGM 60
DB 37 Yfgklesklsvirlnndqvlfidqgnrplfedmtsdcrdnaprtfifismykdsqprgm 96
QY 61 AVTISVKCEKISTLSCENKIISFKEMNPPDNKDKTSDIFFQSVPGHDNKMQFESSY 120
DB 97 avtisivkcekistlscenkilsfkemppdnkdktsdiiffqsvpghdnkmqfessy 156
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
DB 157 egyflacekerdlfkilkkedelgdrsifmftvqned 193

RESULT 12
AAW77082
ID AAW77082 standard; Protein; 193 AA.
XX
AC AAW77082;
XX
DT 16-NOV-1998 (first entry)
XX
DE Interleukin 18 active protein and precursor.
XX
KW Human; interleukin-18; IL-18; osteoclast; hypercalcaemia; osteopenia;
KW osteoclastoma Behcet's syndrome; osteosarcoma; arthropathy; osteoporosis;
KW chronic rheumatoid arthritis; deformity ostitis; primary hyperthyroidism.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..36
FT Peptide /note= "Signal peptide"
FT Peptide 37..193

/note= "Mature peptide"

FT XX EP861663-A2.
PN XX
PD 02-SEP-1998.
XX
PF 24-FEB-1998; 98EP-0301352.
XX
PR 25-FEB-1997; 97JP-0055468.
XX
PA (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
XX
PI Gillespie MT, Horwood NJ, Kurimoto M, Udagawa N;
XX WPI; 1998-448964/39.
XX DR N-PSDB; V4828.
XX
PT Use of interleukin-18 to inhibit osteoclast formation - in treatment
PT of e.g. hypercalcaemia, osteoclastoma, Behcet's syndrome,
PT osteosarcoma, chronic rheumatoid arthritis, deformity ostitis,
PT primary hyperthyroidism and osteoporosis
XX
PS Disclosure; Page 24-28; 56pp; English.
XX
CC Interleukin-18 (IL-18) or a functional equivalent can be used for
CC inhibition of osteoclast formation. IL-18 is used for treating or
CC preventing osteoclast-related diseases e.g. hypercalcaemia, osteoclastoma
CC Behcet's syndrome, osteosarcoma, arthropathy, chronic rheumatoid
CC arthritis, deformity ostitis, primary hyperthyroidism, osteopenia and
CC osteoporosis.
XX
SQ Sequence 193 AA;

Query Match 99.6%; Score 813; DB 19; Length 193;
Best Local Similarity 99.4%; Pred. No. 3.5e-83;
Matches 156; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTFIISMYKDSQPRGM 60
DB 37 Yfgklesklsvirlnndqvlfidqgnrplfedmtsdcrdnaprtfifismykdsqprgm 96
QY 61 AVTISVKCEKISTLSCENKIISFKEMNPPDNKDKTSDIFFQSVPGHDNKMQFESSY 120
DB 97 avtisivkcekistlscenkilsfkemppdnkdktsdiiffqsvpghdnkmqfessy 156
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
DB 157 egyflacekerdlfkilkkedelgdrsifmftvqned 193

RESULT 13
AAR99564
ID AAR99564 standard; Protein; 157 AA.
XX
AC AAR99564;
XX
DT 29-SEP-1996 (first entry)
XX
DE Human interferon-gamma inducer protein.
XX
KW Interferon-gamma inducer protein; IFN-gamma; antiviral; virucide;
KW antitumour; antibacterial; immunoregulator; adoptive immunotherapy;
KW therapy; cancer.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 73
FT /label= Ile, Thr
XX
PN EP712931-A2.
XX
```

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PD 22-MAY-1996.
XX
XX 10-NOV-1995; 95EP-0308055.
XX
XX 29-SEP-1995; 95JP-0274988.
PR 15-NOV-1994; 94JP-0304203.
PR 23-FEB-1995; 95JP-0058240.
PR 10-MAR-1995; 95JP-0078357.
PR 18-SEP-1995; 95JP-0262062.
XX
XX (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
XX
XX Fukuda S, Kohno K, Kunikata T, Kurimoto M, Okamura H;
PI Taniguchi M, Tanimoto T, Torigoe K, Ushio S;
XX
DR WPI; 1996-252837/26.
DR N-PSDB; AAT32411.
XX
XX DNA encoding interferon-gamma prodn.-inducing polypeptide - useful
PT to treat and prevent, e.g. viral disease, malignancies and immune
PT disorders
XX
XX Example B-1-1; Page 28; 48pp; English.
XX
XX A novel human protein (AAR99564) that induces interferon-gamma
CC (IFN-gamma) prodn. by immunocompetent cells is the product of a
CC phage cDNA clone (AAT32411) derived from a human liver library.
CC PCR amplification of the cDNA (see also AAT32409-10) and expression
CC in Escherichia coli XL-1 Blue MRF'kan allowed prodn. of recombinant
CC inducer protein. This was used to construct hybridoma H-1, which
CC produced anti-IFN-gamma inducer protein monoclonal antibody H-1mAb,
CC useful in the detection and purification of the inducer protein
CC (see also AAR99558).
XX
XX Sequence 157 AA;

Query Match 99.4%; Score 811; DB 17; Length 157;
Best Local Similarity 99.4%; Pred. No. 4.5e-83;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPDPEDMTDSCDRNAPRTIFIISMVYKDSQPRGM 60
DB 1 Yfgklesklsvirnlndqvlfidqgnrplfedmtsdcdndnprtifiismykdsgprgm 60
QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDTSKDIFFQFORSVPGHDKMKQFESSY 120
DB 61 avtisvkcekislscenkliisfkemppdnikdtskdiiffqforsvpgdhdkmqfessy 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDGRSIMFTVQNE 157
DB 121 egyflacekerdlfkilkkedelgdrsimftvqned 157

RESULT 14
AAR99558
ID AAR99558 standard; Protein; 157 AA.
XX
XX AAR99558;
XX
XX 29-SEP-1996 (first entry)
DE Human mature interferon-gamma inducer protein.
XX
XX Interferon-gamma inducer protein; IFN-gamma; antiviral; virucide;
KW antitumour; antibacterial; immunoregulator; adoptive immunotherapy;
KW therapy; cancer.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Misc-difference 73
FT /label= Ile, Thr

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XX EP712931-A2.
PN
XX
XX 22-MAY-1996.
PD
XX
XX 10-NOV-1995; 95EP-0308055.
XX
XX 29-SEP-1995; 95JP-0274988.
PR 15-NOV-1994; 94JP-0304203.
PR 23-FEB-1995; 95JP-0058240.
PR 10-MAR-1995; 95JP-0078357.
PR 18-SEP-1995; 95JP-0262062.
XX
XX (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
XX
XX Fukuda S, Kohno K, Kunikata T, Kurimoto M, Okamura H;
PI Taniguchi M, Tanimoto T, Torigoe K, Ushio S;
XX
XX WPI; 1996-252837/26.
DR N-PSDB; AAT32402.
XX
XX DNA encoding interferon-gamma prodn.-inducing polypeptide - useful
PT to treat and prevent, e.g. viral disease, malignancies and immune
PT disorders
XX
XX Claim 1; Page 40; 48pp; English.
XX
XX A novel human protein (AAR99558) induces interferon-gamma (IFN-gamma)
CC prodn. by immunocompetent cells. It enhances the cytotoxicity of
CC killer cells and/or induces the formation of killer cells (e.g.
CC NK cells, lymphokine-activating killer (LAK) cells, and cytotoxic
CC T-cells). Recombinant IFN-gamma inducer protein can be produced in
CC high yields using host cells, esp. Escherichia coli, transformed
CC with a vector carrying the encoding cDNA (AAT32402). It is useful
CC as an antiviral, antitumor, antibacterial, immunoregulatory and
CC blood platelet enhancing agent, and can be used in adoptive
CC immunotherapy. It is also used to raise monoclonal antibodies.
CC A full-length sequence is given in AAR99560.
XX
XX Sequence 157 AA;

Query Match 99.4%; Score 811; DB 17; Length 157;
Best Local Similarity 99.4%; Pred. No. 4.5e-83;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPDPEDMTDSCDRNAPRTIFIISMVYKDSQPRGM 60
DB 1 Yfgklesklsvirnlndqvlfidqgnrplfedmtsdcdndnprtifiismykdsgprgm 60
QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDTSKDIFFQFORSVPGHDKMKQFESSY 120
DB 61 avtisvkcekislscenkliisfkemppdnikdtskdiiffqforsvpgdhdkmqfessy 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDGRSIMFTVQNE 157
DB 121 egyflacekerdlfkilkkedelgdrsimftvqned 157

RESULT 15
AAW15701
ID AAW15701 standard; protein; 157 AA.
XX
XX AAW15701;
XX
XX 26-JAN-1998 (first entry)
DT Interferon-gamma inducer protein.
XX
XX Interferon-gamma, IFN-gamma; antiviral; antioncotic; radiotherapy;
KW immunoregulatory; antitumour agent; chemotherapy; leukopaenia;
KW thrombocytopaenia; immunocompetent cell; asthma; hayfever;
KW rheumatism; interleukin; killer cell.

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XX OS Homo sapiens.
XX FH
XX FT Key Location/Qualifiers
XX FT Misc-difference 73
XX FT /label= Ile, Thr
XX PN
XX PD
XX PF 26-SEP-1996; 96EP-0306997.
XX PR 20-SEP-1996; 96JP-0269105.
XX PR 26-SEP-1995; 95JP-0270725.
XX PR 29-FEB-1996; 96JP-0067434.
XX PA (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
XX PI Akita K, Fujii M, Kurimoto M, Nukada Y, Tanimoto T;
XX DR WPI; 1997-205381/19.
XX PT Human protein that induces interferon-gamma prodn. in
XX PT immuno:competent cells - useful for adoptive immuno:therapy of
XX PT tumours and as antimicrobial agent etc.
XX PS Claim 8; Page 20; 26pp; English.
XX CC
XX CC The present sequence represents a novel protein from human cells, which
XX CC induces interferon-gamma (IFN gamma) production in immunocompetent cells.
XX CC This protein enhances cytotoxicity of killer cells and induces their
XX CC formation. It is used as an antioncotic agent for antitumour
XX CC immunotherapy, an antiviral (including anti-AIDS) or antibacterial agent,
XX CC and in the treatment of atopic or immune system diseases, e.g. asthma,
XX CC hayfever or rheumatism. When formulated with interleukin-3, it is also
XX CC used to treat leukaemia and thrombocytopenia associated with
XX CC radiotherapy or chemotherapy of leukaemia and other cancers. When used in
XX CC antitumour immunotherapy, this novel protein significantly improves the
XX CC immunotherapeutic effect of interleukin-2 (IL-2), compared with use of
XX CC IL-2 alone, either when administered to the patient (before
XX CC administration of IL-2) or by addition to the medium in which cells
XX CC (intended for return to the patient) are being grown.
SQ Sequence 157 AA:

Query Match 99.4%; Score 811; DB 18; Length 157;
Best Local Similarity 99.4%; Pred. No. 4.5e-83;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNPRTIFIIISMYKDSQPRGM 60
   |||||||
Db 1 yfgklesklsvirnlndqvlfidqgnrplfedmtsdcrdnprtifiismykdsqprgm 60
   |||||||

QY 61 AVTISVKCEKISTLSCENKIISFKEMNPPDNIKDKTKSDIIFQRSVPGHDNKMQFESSY 120
   |||||||
Db 61 avtisvkcekisxlscenkilsfkemnpdpnlkctkdsdiiffqrsvpvgnndnkmqfessy 120
   |||||||

QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
   |||||||
Db 121 egyflacekerdlfklikkedelgdrsimftvqned 157
   |||||||
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Search completed: October 8, 2002, 10:15:15
Job time: 276 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 8, 2002, 10:15:51 ; Search time 28.21 seconds
(without alignments)
534.776 Million cell updates/sec

Title: SEQ6THRAT73

Perfect score: 816

Sequence: 1 YFKLESKLSVIRNLNDQVL.....LKKDELGDRSIMFTVQNED 157

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_71.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	520	63.7	192	2 S60226	cytokine IGIF - mo
2	85	10.4	381	2 T40341	hypothetical prote
3	81.5	10.0	270	1 S10532	interleukin-1 alph
4	81	9.9	263	2 T39487	hypothetical prote
5	80.5	9.9	866	2 C71509	probable DNA polym
6	80.5	9.9	1663	1 C3MS	complement C3 prec
7	80	9.8	2470	2 I50726	cation-independent
8	79	9.7	452	2 D64593	hypothetical prote
9	79	9.7	680	2 A28121	major merozoite su
10	79	9.7	1772	2 A45532	hypothetical prote
11	78.5	9.6	204	2 T44357	hypothetical prote
12	78	9.6	473	2 T32038	hypothetical prote
13	77.5	9.5	1251	2 A56677	neuronal cell cycl
14	77	9.4	364	2 A81261	probable periplasm
15	76.5	9.4	425	2 T25457	hypothetical prote
16	76	9.3	632	2 T00679	hypothetical prote
17	76	9.3	747	2 E84698	hypothetical prote
18	75.5	9.3	192	2 S15661	(3'-5')oligo(A) sy
19	75.5	9.3	270	2 I46620	interleukin-1 alph
20	75.5	9.3	467	2 A48713	serine/threonine-s
21	75.5	9.3	578	2 H82872	hypothetical prote
22	75	9.2	467	2 T49609	proto-oncogene pro
23	74.5	9.1	1064	1 S57450	protein-tyrosine k
24	74.5	9.1	334	2 T04198	hypothetical prote
25	74.5	9.1	351	2 E71372	probable translati
26	74.5	9.1	1036	2 H64245	hypothetical prote
27	74.5	9.1	1228	2 A57384	multimerin, endoth
28	74.5	9.1	1510	2 T16927	hypothetical prote
29	74	9.1	245	2 B90488	hypothetical prote

30	74	9.1	361	2 E96904	minD family ATPase
31	74	9.1	376	2 T24925	hypothetical prote
32	74	9.1	467	2 A47388	serine/threonine p
33	74	9.1	810	2 B71639	virb4 protein prec
34	74	9.1	2663	1 S28261	centromere protein
35	73.5	9.0	268	2 H85641	probable small sub
36	73.5	9.0	268	2 C90781	probable small sub
37	73.5	9.0	389	2 B69277	TRK potassium upa
38	73.5	9.0	432	2 G90268	conserved hypothet
39	73.5	9.0	475	2 T32036	hypothetical prote
40	73.5	9.0	888	2 A38539	p101 protein precu
41	73.5	9.0	1997	2 F71607	DNA helicase II BR
42	73	8.9	418	2 D82932	seryl-tRNA synthet
43	73	8.9	447	2 T26293	hypothetical prote
44	72.5	8.9	268	1 ICB01A	interleukin-1 alph
45	72.5	8.9	268	1 B24073	interleukin-1 alph

ALIGNMENTS

RESULT 1

S60226

cytokine IGIF - mouse

C:Species: Mus musculus (house mouse)

C:Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 20-Jun-2000

C:Accession: S60226

R:Okamura, H.; Tsutsui, H.; Komatsu, T.; Yutsudo, M.; Hakura, A.; Tanimoto, T.; Torig

Nature 378, 88-91, 1995

A:Title: Cloning of a new cytokine that induces IFN-gamma production by T cells.

A:Reference number: S60226; MUID:96061009

A:Accession: S60226

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-192 <OKA>

A:Cross-references: EMBL:D49949; NID:g1064822; PIDN:BAA08705.1; PID:g1064823

C:Superfamily: Mus musculus cytokine IGIF

Query Match

Best Local Similarity

Matches 101; Conservative 27; Mismatches 24; Indels 2; Gaps 2;

Qy 2 FGKLESKLSVIRNLNDQVLFDQGNRPLFEDMTSDCRONAPRTIFIIISMYKDSQPRGMA 61

Db 37 FGRLHCTTAVIRNLNDQVLFDVK-RQPVFEDMTDIDQSAEPQTRLIIIMYKDSVIRGLA 95

Qy 62 VTISVKCEKISLSCENKIIISFKEMNPPDNIKDTKSDIIFQORSVPGHDKMKQFESSSYE 121

Db 96 VTLVKDKSKMTLSCKNKIIISFEEMDPDENIDDDIQSDLIFFQKRVPGH-NKMEFESSLYE 154

Qy 122 GYFLACERDLFKLILKKEDELGDRSIMFTVQN 155

Db 155 GHFLACQKDEADFKLILKKEDELGDRSIMFTITN 188

RESULT 2

T40341

hypothetical protein SPBC3B9.02c - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999

C:Accession: T40341

R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M.

submitted to the EMBL Data Library, March 1997

A:Reference number: Z21922

A:Accession: T40341

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-381 <WOO>

A:Cross-references: EMBL:AL0202070; PIDN:CAAL17782.1; GSPDB:GN00067; SPDB:SPBC3B9.02c

A:Experimental source: strain 972h-; cosmid c3B9

C:Genetics:

A; Cross-references: GB:M3032; NID:gl92391; PIDN:AAA37378.1; PID:gl92392
C; Comment: Complement C3 contains two chains, formed by removal of four residues and alternative complement pathways, releases the C3a anaphylatoxin from the amino end of native-complement-pathway C3/C5 convertase.
C; Comment: C3a anaphylatoxin is a vasoactive peptide and a mediator of inflammation..
C; Comment: C3b, with its highly reactive thiol group, binds to the surface of foreign e classical-complement-pathway C3/C5 convertase. The activity of C3b is regulated by C; Comment: The major site of synthesis of this plasma protein is the liver.
C; Genetics:
A; Introns: 27/2; 90/3
A; Note: the list of introns may be incomplete
C; Superfamily: alpha-2-macroglobulin
C; Keywords: acute phase; complement alternate pathway; complement pathway; glycoprotein
F; 1-24/Domain: signal sequence #status predicted <SIG>
F; 25-666/Product: complement C3 and C3b beta chain #status predicted <C3BB>
F; 25-666,671-1663/Product: complement C3 #status predicted <CC3>
F; 25-666,749-1663/Product: C3b #status predicted <C3B>
F; 671-1663/Product: complement C3 alpha chain #status predicted <CC3A>
F; 671-748/Product: C3a anaphylatoxin #status predicted <C3T>
F; 749-1663/Product: C3b alpha' chain #status predicted <C3BA>
F; 946-1303/Product: C3dk fragment #status predicted <CDK>
F; 1002-1303/Product: C3d fragment #status predicted <CDK>
F; 1424-1457/Region: propeptide binding
F; 559-816,626-661,693-720,694-727,707-728,873-1513,1101-1158,1358-1489,1389-1458,1506
F; 748-749/Cleavage site: Arg-Ser (C3 convertase) #status predicted
F; 749-1617/Binding site: carbohydrate (Asn) (covalent) #status predicted
F; 1010-1013/cross-link: thiolester (Cys-Gln) #status predicted
F; 1303-1304/Cleavage site: Arg-Ser (complement factor I) #status predicted
F; 1320-1321/Cleavage site: Arg-Ser (complement factor I) #status predicted

Query Match 9.9%; Score 80.5; DB 1; Length 1663;
Best Local Similarity 24.1%; Pred. No. 35;
Matches 26; Conservative 23; Mismatches 44; Indels 15; Gaps 4;

QY 18 QVLFIDGN--RPLFDMTDSDCRDNAPRT-----IFIISMVKDSQPMGMAVTISVKCEKI 71
DB 387 KVLVVTOGSNAKALTDDGVAKLSINTPSNRQP LTIIVRTKKDTLPESROATKTMEAHPY 446
QY 72 STLSCENKI---ISFEMNPNNIKDKTSIDIIFQRSVPGHONKMOF 115
DB 447 STHINSNNYLHLVSRELKPGDNL-----NVNPHLRTDFGHEAKIRY 489

RESULT 7
I50726
cation-independent mannose-6-phosphate receptor - chicken
C; Species: Gallus gallus (chicken)
C; Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 20-Aug-1999
C; Accession: I50726
R; Zhou, M.; Ma, Z.; Sly, W.S.
Proc. Natl. Acad. Sci. U.S.A. 92, 9762-9766, 1995
A; Title: Cloning and expression of the cDNA of chicken cation-independent mannose-6-p
A; Reference number: I50726; MUID:96003859
A; Accession: I50726
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-2470 <ZHO>
A; Cross-references: EMBL:U35037; NID:g1019118; PIDN:AAC59718.1; PID:g1019119
C; Superfamily: mannose 6-phosphate receptor, cation-independent; fibronectin type II
F; 1882-1921/Domain: fibronectin type II repeat homology <2FI>

Query Match 9.8%; Score 80; DB 2; Length 2470;
Best Local Similarity 25.9%; Pred. No. 62;
Matches 45; Conservative 30; Mismatches 51; Indels 48; Gaps 12;

QY 4 KLESKSLVIRNLND--QVLFIDQGNRPLEDMTDSDCRDNAPRT--IFIISMVK----- 53
DB 1457 KIESKP ELIMAIEDCEYSFWFTAAACPL-KSNVQNDCRVNPNPATGHFLDLTSLKRESGY 1515
QY 54 ---DSQPR-----GMAVTI-----SVKCEKIS--TLSCENKIIS--EKEM 86

```

Db      217 EQYKELLPGK--VTVSTPAVAVTTLAADAPATPEGAVPGAVPGAVPGAV--PCGV 272
          ||| :|| |:|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Qy      107 PGHDNKKMFESSYEGYFLACAKERDLFKLILKEDELGDRSIMFTVQNE 156
          ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db      273 PGSCTDTRFVAGSSVDD-----NEDDDIIQIASGQSEDAPEKDILSEPTNE 317

RESULT 10
A45532
major merozoite surface antigen precursor - Plasmodium yoelii
C:Species: Plasmodium yoelii
C:date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 26-Aug-1999
C:Accession: A45532; MUID:90014981
R:Lewis, A.P.
Mol. Biochem. Parasitol. 36, 271-282, 1989
A:title: Cloning and analysis of the gene encoding the 230-kilodalton merozoite surfa
A:Reference number: A45532; MUID:90014981
A:Accession: A45532
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1772 <LEW>
A:Cross-references: GB:J04668; NID:g160492; PID:g160493
R:Daly, T.M.; Burns Jr., J.M.; Long, C.A.
Mol. Biochem. Parasitol. 36, 283-285, 1989
A:title: Precursor to the major merozoite surface antigen of Plasmodium yoelii: clon
A:Reference number: A45531; MUID:90014982
A:Accession: A45531
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 454-1094 <DAL>
A:Cross-references: GB:J03975; NID:g160081; PID:g160082
C:Superfamily: major merozoite surface antigen
C:Keywords: surface antigen

Query Match          9.7%; Score 79; DB 2; Length 1772;
Best Local Similarity 19.4%; Pred. No. 52;
Matches 33; Conservative 36; Mismatches 75; Indels 26; Gaps 7;

Qy      2 FGKLESKLIVRNLN---DOVLFDGGRPLFE-----DMTSDSCRDNPARTIFII 49
          ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db      1251 YSRLELRK--KNINLGKRISVGGHLHFVEEFKELIKDKOYTGKKNDPNAPEVTNAF 1308

Qy      50 SMYKDSOPRGMAVTISKVKBKISLCSENKIISFKENP---PDNIKDTKSDIFFORSV 106
          ||| :|| |:|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db      1309 EQYKELLPGK--VTVSTPAVAVTTLAADAPATPEGAVPGAVPGAVPGAV--PCGV 1364

Qy      107 PGHDNKKMFESSYEGYFLACAKERDLFKLILKEDELGDRSIMFTVQNE 156
          ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db      1365 PGSCTDTRFVAGSSVDD-----NEDDDIIQIASGQSEDAPEKDILSEPTNE 1409

RESULT 11
T44357
hypothetical protein [imported] - Clostridium histolyticum
C:Species: Clostridium histolyticum
C:date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C:Accession: T44357
R:Watsushita, O.; Jung, C.M.; Katayama, S.; Minami, J.; Takahashi, Y.; Okabe, A.
J. Bacteriol. 181, 923-933, 1999
A:title: Gene duplication and multiplicity of collagenases in Clostridium histolyticu
A:Reference number: 222752; MUID:99121032
A:Accession: T44357
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-204 <MAT>
A:Cross-references: EMBL:AB014075; NID:g3868863; PIDN:BAA34544.1; PID:g3892648
A:Experimental source: strain JCM 1403

Query Match          9.6%; Score 78.5; DB 2; Length 204;
Best Local Similarity 26.4%; Pred. No. 4.5;

```

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A; Note: conceptual translation not given
```

		9.5%;	Score 77.5;	DB 2;	Length 1251;
	Query Match				
	Best Local Similarity	23.5%;	Pred. No. 48;		
	Matches 38; Conservative 37; Mismatches 64; Indels 23; Gaps 9;				
QY	6	ESKLSVI-RNLNDQVLFI---	DGNGRPLFEDMTDSCRDNAPRTIFII	SNYKDSQPRGMA	61
		: : : : : :	: : :	: : :	
Db	648	EELAQIQREMEDQEVIIQGYQENRLYKOMKDLOIQNKNEE----	OMYKENOCL-MS	702	
		: : : : : :	: : :	: : :	
QY	62	VTSVRCEKITSLSCENKIISFKEMNPPNIKDTKSIDIFFORSVFGHDKWFOE-----	116		
		: : : : : :	: : :	: : :	

```

Qy 117 --SSSEGYFLACEKERDLPKLLKKEDELGDRSIMFTVQNE 156
      :
      :||||| : :
      :||| : :
Db 758 QDRQALELDLGAKKERDLAKVQITSTS--SEKSYEFKIMEE 797
      :
      :||| : :
      :||| : :

RESULT 14
A:probable periplasmic protein Cj1643 [imported] - Campylobacter jejuni (strain NCTC 11
A:18261
C:Species: Campylobacter jejuni
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 31-Mar-2000
R:C:Accession: A81261
R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chil
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVleet, A.; Whitehead, S.; Ba
Nature 403, 665-668, 2000
A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals
A:Reference number: A81250; WUID:20150912
A:Accession: A81261
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-364 <PAR>
A:Cross-references: GB:AL139079; GB:AL111168; NID:g6968971; PIDN:CAB73631.1; PID:g696
A:Experimental source: serotype O2, strain NCTC 11168
C:Genetics:
A:Gene: Cj1643

```

[illegible]

RESULT 15
T25457
hypothetical protein B0432.9 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Sep-2000
C:Accession: T25457
R:Henkhaus, J.; Wohldmann, P.
submitted to the EMBL data Library, December 1996
A:Description: The sequence of *C. elegans* cosmid B0432.
A:Reference number: Z20038
A:Accession: T25457
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-425 <HEN>
A:Cross-references: EMBL:U080836; PIDN:AA837893.1; GSPD:GN000020; CESP:B0432.9

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 8, 2002, 10:17:03 ; Search time 15.78 Seconds
(without alignments)
385.233 Million cell updates/sec

Title: SEQ6THRAT73

Perfect score: 816

Sequence: 1 YFGKLESKSLVIRNLNDQVL.....LKKDELGDRSIMFTVQNE 157

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	816	100.0	193	IL18_HUMAN	Q14116 homo sapien
2	664	81.4	193	IL18_HORSE	Q9Xsq7 equus cabal
3	659	80.8	193	IL18_BOVIN	Q9tu73 bos taurus
4	642	78.7	192	IL18_PIG	O19073 sus scrofa
5	618	75.7	193	IL18_CANFA	Q9Xsr0 canis famil
6	520	63.7	192	IL18_MOUSE	P07380 mus musculu
7	519.5	63.7	194	IL18_RAT	P97636 rattus norv
8	81.5	10.0	270	IL1A_PIG	P18430 sus scrofa
9	81	9.9	267	IL1A_RABIT	P04822 oryctolagus
10	80.5	9.9	1663	C03_MOUSE	P01027 mus musculu
11	79	9.7	1772	MSPI_PLAYO	P13828 plasmodium
12	77.5	9.5	270	IL1A_HORSE	Q28385 equus cabal
13	75.5	9.3	192	ORAB_MOUSE	Q60856 mus musculu
14	75	9.2	467	M3K8_MOUSE	Q07174 mus musculu
15	74.5	9.1	351	RF1_TREPA	O83090 treponema p
16	74.5	9.1	1036	Y141_MYCGE	P47653 mycoplasma
17	74.5	9.1	1228	ECM_HUMAN	Q13201 homo sapien
18	74	9.1	270	IL1A_FELCA	O46613 felis silve
19	74	9.1	467	M3K8_RAT	Q63562 rattus norv
20	74	9.1	2663	CENE_HUMAN	Q02224 homo sapien
21	73	8.9	4590	FATH_HUMAN	Q14517 homo sapien
22	72.5	8.9	268	IL1A_BOVIN	P08831 bos taurus
23	72.5	8.9	313	COLA_ARATH	Q9m9b3 arabidopsis
24	72.5	8.9	467	M3K8_HUMAN	P41279 homo sapien
25	72	8.8	426	YXCX_ASTLO	P8151 astasia ion
26	72	8.8	700	NONA_DROME	Q04047 drosophila
27	72	8.8	800	K1N4_YEAST	Q01919 saccharomyc
28	71.5	8.8	268	IL1A_CAPHI	P79161 capra hircu
29	71.5	8.8	375	YVC5_CAEEL	Q18610 caenorhabdi
30	71.5	8.8	377	NCK1_HUMAN	P16333 homo sapien
31	71.5	8.8	527	RAG2_HUMAN	P55895 homo sapien
32	71	8.7	198	V511_ROTNA	P17467 rabbit rota
33	70.5	8.6	268	IL1A_SHEEP	Q28579 ovine aries

34	70.5	8.6	642	1	FLID_CAMJE	O9phw6 campylobact
35	70.5	8.6	704	1	YGZ9_YEAST	P53061 saccharomyc
36	70.5	8.6	1091	1	ITAG_MOUSE	Q61739 mus musculu
37	70.5	8.6	1230	1	SMC3_YEAST	P47037 saccharomyc
38	70	8.6	451	1	VPS9_YEAST	P25787 saccharomyc
39	70	8.6	1486	1	MUKB_ECOLI	P22523 escherichia
40	70	8.6	1647	1	SN24_HUMAN	P51532 homo sapien
41	69.5	8.5	582	1	CRTI_CAPAN	P80093 capsicum an
42	69.5	8.5	644	1	YGM4_YEAST	P53129 saccharomyc
43	69.5	8.5	919	1	RFO2_CAPVK	P16716 capripoxvir
44	69	8.5	492	1	UBID_PASMR	Q9cp43 pasteurella
45	69	8.5	578	1	TRM1_DROME	Q9vkh8 drosophila

ALIGNMENTS

RESULT	1
IL18_HUMAN	
ID	IL18_HUMAN STANDARD; PRT; 193 AA.
AC	Q14116; 075599;
DT	15-JUL-1998 (Rel. 36, Created)
DF	15-JUL-1998 (Rel. 36, Last sequence update)
DE	01-MAR-2002 (Rel. 41, Last annotation update)
DE	Interleukin-18 precursor (IL-18) (Interferon-gamma inducing factor)
DE	(IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).
GN	IL18 OR IGIF.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Liver;
RX	MEDLINE=96247646; PubMed=8666798;
RA	Ushio S., Namba M., Okura T., Hattori K., Nukada Y., Akita K.,
RA	Tanabe F., Konishi K., Micallef M., Fujii M., Torigoe K., Tanimoto T.,
RA	Fukuda S., Ikeda M., Okamura H., Kurimoto M.;
RT	"Cloning of the cDNA for human IFN-gamma-inducing factor, expression
RT	in Escherichia coli, and studies on the biologic activities of the
RT	protein.";
RL	J. Immunol. 156:4274-4279(1996).
RN	[2]
RP	SEQUENCE FROM N.A.
RA	Yong D., Guixin D., Lihua H., Haitao W.;
RT	"Cloning and sequencing of the cDNA for precursor hIL-18.";
RT	Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN	[3]
RP	SEQUENCE FROM N.A.
RA	Liu J., Peng X., Yuan J., Qiang B.;
RT	"Cloning of human interleukin 18 cDNA.";
RL	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN	[4]
RP	SEQUENCE OF 2-193 FROM N.A.
RC	TISSUE=Periphereal blood;
RA	Conti B., Kim S.J., Tinti C., Chun H.S., Joh T.H.;
RL	Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC	-!- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
CC	AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CC	CELLS.
CC	-!- SUBCELLULAR LOCATION: Secreted.
CC	-!- SIMILARITY: BELONGS TO THE IL-18 FAMILY.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC	the European Bioinformatics Institute. There are no restrictions on its
CC	use by non-profit institutions as long as its content is in no way
CC	modified and this statement is not removed. Usage by and for commercial
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC	or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL; D49950; BAA08706.1; -.
DR	EMBL; AF077611; AAC27787.1; -.

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DR EMBL; AY04641; AAK95950.1; -.
DR EMBL; U90434; AAB50010.1; -.
DR MIM; 600953; -.
DR InterPro; IPR000975; Interleukin_1.
DR SMART; SM00125; IL1; 1.
KW Cytokine.
FT PROPEP 1 36 BY SIMILARITY.
FT CHAIN 37 193 INTERLEUKIN-18.
FT PROPEP 37 193 INTERLEUKIN-18.
FT CONFLICT 66 66 F -> L (IN REF. 2).
FT CONFLICT 86 86 S -> R (IN REF. 2).
FT CONFLICT 191 191 N -> S (IN REF. 2).
FT CONFLICT 191 191 N -> S (IN REF. 2).
SQ SEQUENCE 193 AA; 22326 MW; 323C62C203788D55 CRC64;

Query Match 100.0%; Score 816; DB 1; Length 193;
Best Local Similarity 100.0%; Pred. No. 1.6e-68;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSCDRNAPRTTIFIISMVKDSQPRGM 60
DB 37 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSCDRNAPRTTIFIISMVKDSQPRGM 96

QY 61 AVTISVKCEKISTLSCENKIIISFKEMNPPDNIDKTSDIFFORSVPGHDKNQFESSY 120
DB 97 AVTISVKCEKISTLSCENKIIISFKEMNPPDNIDKTSDIFFORSVPGHDKNQFESSY 156

QY 121 EGYFLACEKERDLFKILKKEDELGDRSIMFTVQNE 157
DB 157 EGYFLACEKERDLFKILKKEDELGDRSIMFTVQNE 193

RESULT 2
IL18_HORSE
ID IL18_HORSE STANDARD; PRT; 193 AA.
AC QXQSQT;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE Interleukin-18 precursor (IL-18) (Interleukin-18)
DE (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).
GN IL18 OR IGIF.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Nicolson L., Penha-Goncalves M.N., Keanie J.L., Logan N.A.,
RA Argyle D.J., Onions D.E.;
RT "Nucleotide sequence of equine interleukin 12 and 18 cDNAs.";
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CC CELLS (BY SIMILARITY).
CC EMBL; AF124789; AAF08686.1; -.
CC InterPro; IPR000975; Interleukin_1.
CC SMART; SM00125; IL1; 1.
CC Cytokine.
FT PROPEP 1 36 BY SIMILARITY.
FT CHAIN 37 193 INTERLEUKIN-18.
SQ SEQUENCE 193 AA; 22058 MW; 4D81535E9004ECAF CRC64;

Query Match 81.4%; Score 664; DB 1; Length 193;
```

```
Best Local Similarity 78.3%; Pred. No. 1.7e-54;
Matches 123; Conservative 21; Mismatches 13; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSCDRNAPRTTIFIISMVKDSQPRGM 60
DB 37 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSCDRNAPRTTIFIISMVKDSQPRGM 96

QY 61 AVTISVKCEKISTLSCENKIIISFKEMNPPDNIDKTSDIFFORSVPGHDKNQFESSY 120
DB 97 AVTISVKCEKISTLSCENKIIISFKEMNPPDNIDKTSDIFFORSVPGHDKNQFESSY 156

QY 121 EGYFLACEKERDLFKILKKEDELGDRSIMFTVQNE 157
DB 157 EGYFLACEKERDLFKILKKEDELGDRSIMFTVQNE 193

RESULT 3
IL18_BOVIN
ID IL18_BOVIN STANDARD; PRT; 193 AA.
AC Q9TU73;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Interleukin-18 precursor (IL-18) (interleukin-gamma inducing factor)
DE (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).
GN IL18.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20012648; PubMed=10547157;
RA Shoda L.K., Zarlenga D.S., Hirano A., Brown W.C.;
RT "Cloning of a cDNA encoding bovine interleukin-18 and analysis of IL-
RT 18 expression in macrophages and its IFN-gamma-inducing activity.";
RL J. Interferon Cytokine Res. 19:1169-1177(1999).
CC -1- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CC CELLS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE IL-18 FAMILY.
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CC or send an email to license@isb-sib.ch).
CC EMBL; AF124789; AAF08686.1; -.
CC InterPro; IPR000975; Interleukin_1.
CC SMART; SM00125; IL1; 1.
CC Cytokine.
FT PROPEP 1 36 BY SIMILARITY.
FT CHAIN 37 193 INTERLEUKIN-18.
SQ SEQUENCE 193 AA; 22347 MW; 65720F199DEA49C4 CRC64;

Query Match 80.8%; Score 659; DB 1; Length 193;
Best Local Similarity 77.7%; Pred. No. 4.9e-54;
Matches 122; Conservative 23; Mismatches 12; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSCDRNAPRTTIFIISMVKDSQPRGM 60
DB 37 HFGKLEPKLSIIRNLNDQVLFIDQGNRPLFEDMTDSCDRNAPRTTIFIISMVKDSQPRGM 96

QY 61 AVTISVKCEKISTLSCENKIIISFKEMNPPDNIDKTSDIFFORSVPGHDKNQFESSY 120
DB 97 AVTISVCKRMSTLSCENKIVSFEMNPPDNIDNEESDIIFORSVPGHDKNQFESSY 156
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=96061009; PubMed=7477296;
RA Okamura H., Tsutui H., Komatsu T., Yutsudo M., Hakura A.,
RA Tanimoto T., Torigoe K., Okura T., Nakada Y., Hattori K.,
RA Akita K., Namba M., Tanabe F., Konishi K., Fukuda S., Kurimoto M.;
RA "Cloning of a new cytokine that induces IFN-gamma production by T
RT cells.";
RT Nature 378:88-91(1995).
RN [2]
RN SEQUENCE OF 1-191 FROM N.A.
RP STRAIN=NOD; TISSUE=Pancreas;
RX MEDLINE=97174346; PubMed=9022080;
RA Roche H., Jenkins N.A., Copeland N.G., Kolb H.;
RA "Active stage of autoimmune diabetes is associated with the
RT expression of a novel cytokine, IGIF, which is located near Idd2.";
RL J. Clin. Invest. 99:469-474(1997).
CC -1- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE 1
CC CELLS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE IL-18 FAMILY.
CC -----
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CC -----
DR EMBL; D49949; BAA08705.1; -.
DR EMBL; U66244; AAB49753.1; -.
DR MGD; MGI:107936; IL18.
DR InterPro: IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR SMART; SM00125; IL1; 1.
KW Cytokine.
FT PROPEP 1 35
FT CHAIN 36 192 INTERLEUKIN-18.
FT CONFLICT 183 185 MFT -> IS (IN REF. 2).
FT SEQUENCE 192 AA; 22135 MW; 8FED938473874D63 CRC64;
SQ
Query Match 63.7%; Score 520; DB 1; Length 192;
Best Local Similarity 65.6%; Pred. No. 3.3e-41;
Matches 101; Conservative 27; Mismatches 24; Indels 2; Gaps 2;
QY 2 FGKLESKLSVIRNLNDQVLFIDGQNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGMA 61
Db 37 FGRUHCCTAVIRNLNDQVLFVDK-RQPVFEDMTDIDQASPEQTRLIIYMYKDSVGRGLA 95
QY 62 VTISVCKEISTLSCENKIISFKEMNPPDNKDKTSIDIFFQRSVPCHDNKMQFESSY 121
Db 96 VTLSVKDSKMSLTSCNKNKIISFEEMDPENIDDIQSDLIFFQKRVPGH-NKMEFESSLYE 154
QY 122 GYFLACEKERDLFKLILKKEDELGDRSIMFTVQN 155
Db 155 GHFLACQKEDDAFLKILKKEDELGDKSVMTLTN 188
RESULT 7
ID IL18_RAT STANDARD; PRT; 194 AA.
AC P97636; P97637; O88749;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-18 precursor (IL-18) (interferon-gamma inducing factor)

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DE (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).
GN IL18 OR IGIF.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=SPRAGUE-DAWLEY; TISSUE=Adrenal gland;
RX MEDLINE=97152963; PubMed=8998986;
RA Conti B., Jahng J.W., Tinti C., Son J.H., Joh T.H.;
RA "Induction of interferon-gamma inducing factor in the adrenal
RT cortex.";
RT J. Biol. Chem. 272:2035-2037(1997).
RN [2]
RN SEQUENCE FROM N.A.
RP STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain;
RX MEDLINE=98368130; PubMed=9702748;
RA Culhane A.C., Hall M.D., Rothwell N.J., Luheshi G.N.;
RA "Cloning of rat brain interleukin-18 cDNA.";
RL Mol. Psych. 3:362-366(1998).
CC -1- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE 1
CC CELLS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE IL-18 FAMILY.
CC -----
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CC -----
DR EMBL; U77776; AAC53009.1; -.
DR EMBL; U77777; AAC53010.1; -.
DR EMBL; AJ222813; CAA11001.1; -.
DR InterPro: IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR SMART; SM00125; IL1; 1.
KW Cytokine; Alternative splicing.
FT PROPEP 1 36 BY SIMILARITY.
FT CHAIN 37 194 INTERLEUKIN-18.
FT VARSPLIC 121 139 MISSING (IN ISOFORM ALPHA).
FT CONFLICT 4 5 MS -> TP (IN REF. 2).
FT CONFLICT 48 48 I -> M (IN REF. 2).
FT SEQUENCE 194 AA; 22303 MW; E2089AD6F1798450 CRC64;
SQ
Query Match 63.7%; Score 519.5; DB 1; Length 194;
Best Local Similarity 63.9%; Pred. No. 3.7e-41;
Matches 99; Conservative 28; Mismatches 27; Indels 1; Gaps 1;
QY 1 YFGKLESKLSVIRNLNDQVLFIDGQNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
Db 37 HFGRUHCCTAVIRNLNDQVLFVDKRNPPVFPEDMPDIDRTANESQTRLIIYMYKDSVRGL 96
QY 61 AVTISVCKEISTLSCENKIISFKEMNPPDNKDKTSIDIFFQRSVPCHDNKMQFESSY 120
Db 97 AVTUSVKDGRMSTLSCNKNKIISFEEMNPPENIDDIKSLIFFQKRVPGH-NKMEFESSLY 155
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQN 155
Db 156 EGFLACQKEDDAFLKILKKEDELGDKSVMTLTN 190
RESULT 8
ID IL1A_PIG STANDARD; PRT; 270 AA.
AC P18430;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)

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DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Interleukin-1 alpha precursor (IL-1 alpha).
GN IL1A.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung.
RX MEDLINE=90332454; PubMed=2377484;
RA Maliszewski C.R., Renshaw B.R., Schoenborn M.A., Urban J.F.,
RA Baker P.E.;
RT "Porcine IL-1 alpha cDNA nucleotide sequence.";
RL Nucleic Acids Res. 18:4282-4282(1990).
RN [2]
RP SEQUENCE FROM N.A.
RA Huecher M.J., Scamurra R.W., Murtaugh M.P., Molitor T.W.;
RL Submitted (XX-1992) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
CC -!- SUBUNIT: MONOMER.
CC -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC -!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC SECRETORY PROTEINS.
CC -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC -----
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CC -----
DR EMBL; X52731; CAA36945.1; -
DR EMBL; M86730; AAA73198.1; -
DR PIR; S10532; S10532.
DR HSP; P01583; LITA.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR PRINTS; PR00264; INTERLEUKIN1.
DR SMART; SM00125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; 1.
KW Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
FT PROPEP 1 112
FT CHAIN 113 270 INTERLEUKIN-1 ALPHA.
FT CARBOHYD 102 102 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 89 89 N -> I (IN REF. 2).
FT CONFLICT 242 242 F -> L (IN REF. 2).
FT CONFLICT 255 255 P -> R (IN REF. 2).
SQ SEQUENCE 270 AA; 30788 MW; 5677BF2B0EF63839 CRC64;

Query Match
Best Local Similarity 10.0%; Score 81.5; DB 1; Length 270;
Matches 28; Conservative 34; Mismatches 58; Indels 11; Gaps 5;

QY 8 KLSVIRNLNDQVLFIDQGNRPLFEDMTD----SDCRDNAPRTI-FTISMVKDSQPRGMV 62
DB 123 KYNFMRVINHQCILNDARNQSIIRDPSGQYLMAVLNNLDEAVKFDMAAYTSDNDSQLPV 182
QY 63 TISVKCEKI-STLSCENKIISFKEM-NPPDNIKDKTSKDIIFQSRVPGHDKMKQFESSY 120
DB 183 TLRISETRLFVSAONEDPVLKELPTKTKIDETSLFFWEK----HGNMDYFKSAAH 238
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QY 121 EGYFLACEKER 131
DB 239 PKLFATATROEK 249

RESULT 9
IL1A_RABIT STANDARD; PRT; 267 AA.
ID IL1A_RABIT
AC P04822;
DT 13-AUG-1987 (Rel. 05, Created)
DT 15-AUG-1987 (Rel. 05, Last sequence update)
DT 13-DEC-1998 (Rel. 37, Last annotation update)
DE Interleukin-1 alpha precursor (IL-1 alpha).
GN IL1A.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85297782; PubMed=2994016;
RA Furutani Y., Notake M., Yamayoshi M., Yamagishi J., Nomura H.,
RA Ohue M., Furuta R., Fukui T., Yamada M., Nakamura S.;
RT "Cloning and characterization of the cDNAs for human and rabbit
RT Interleukin-1 precursor.";
RL Nucleic Acids Res. 13:5869-5882(1985).
CC -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
CC -!- SUBUNIT: MONOMER.
CC -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC -!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC SECRETORY PROTEINS.
CC -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC -----
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CC -----
DR EMBL; X02852; CAA26605.1; -
DR PIR; B24073; B24073.
DR HSP; P01583; LITA.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR PRINTS; PR00264; INTERLEUKIN1.
DR SMART; SM00125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; 1.
KW Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
FT PROPEP 1 112
FT CHAIN 113 267 INTERLEUKIN-1 ALPHA.
FT CARBOHYD 64 64 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 267 AA; 30375 MW; 6D20533FD1FA4822 CRC64;

Query Match
Best Local Similarity 9.9%; Score 81; DB 1; Length 267;
Matches 31; Conservative 27; Mismatches 58; Indels 10; Gaps 4;

QY 12 IRLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTI-----FIISMVKDSQPRGMV 66
```

Db 127 LRIKQETFLDALNQSLVRLSDQYLRAAPLQNLGDAVKFMDGYMTSEDSILPVLRI 186
 QY 67 -KCEKISLSCENKIIFKEM-NPNDINKDKPSDLIEFORSVPGHDKNKMPSESSYECYF 124
 Db 187 SQTPLFVSAQNEDEPVLVKEMPTPRIITDSSEDLFFWET---QGNKNYKPSAANPOLF 243
 QY 125 LACEKE 130
 Db 244 IATKPE 249
 RESULT 10
 CO3_MOUSE STANDARD; PRT; 1663 AA.
 AC P01027;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Complement C3 precursor (HSE-MSF) [Contains: C3A anaphylatoxin].
 GN C3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=65038854; PubMed=6208565;
 RA Fey G.H., Lundwall A., Wessel R.A., Tack B.F., de Bruijn M.H.L.,
 RA Domdey H.;
 RT "Nucleotide sequence of complementary DNA and derived amino acid
 RT sequence of murine complement protein C3";
 RL Philos. Trans. R. Soc. Lond., B, Biol. Sci. 306:333-344(1984).
 RN [2]
 RP SEQUENCE OF 671-1663 FROM N.A.
 RX MEDLINE=6504819; PubMed=6094532;
 RA Wessel R.A., Lundwall A., Davidson P., Gibson T., Tack B.F., Fey G.H.;
 RA Domdey H., Wiebauer K., Kazmaier M., Mueller V., Odink K., Fey G.H.;
 RT "Structure of murine complement component C3. II. Nucleotide sequence
 RT of cloned complementary DNA coding for the alpha chain";
 RL J. Biol. Chem. 259:13857-13862(1984).
 RN [3]
 RP SEQUENCE OF 671-748 FROM N.A.
 RX MEDLINE=83117730; PubMed=6961437;
 RA Domdey H., Wiebauer K., Kazmaier M., Mueller V., Odink K., Fey G.H.;
 RA Domdey H., Wiebauer K., Kazmaier M., Mueller V., Odink K., Fey G.H.;
 RT "Characterization of the mRNA and cloned cDNA specifying the third
 RT component of mouse complement";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:7619-7623(1982).
 RN [4]
 RP SEQUENCE OF 658-761 FROM N.A.
 RX MEDLINE=84201365; PubMed=6609661;
 RA Fey G.H., Wiebauer K., Domdey H.;
 RA "Amino acid sequences of mouse complement C3 derived from nucleotide
 RT sequences of cloned cDNA";
 RL Ann. N.Y. Acad. Sci. 421:307-312(1983).
 RN [5]
 RP SEQUENCE OF 1-34 FROM N.A.
 RX MEDLINE=83117622; PubMed=6985486;
 RA Wiebauer K., Domdey H., Diggelmann H., Fey G.;
 RA "Isolation and analysis of genomic DNA clones encoding the third
 RT component of mouse complement";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:7077-7081(1982).
 RN [6]
 RP SEQUENCE OF 25-41 AND 749-760.
 RX MEDLINE=93373334; PubMed=8364938;
 RA Hamada J.-I., Cavanaugh P.G., Miki K., Nicolson G.L.;
 RA "A paracrine migration-stimulating factor for metastatic tumor cells
 RT secreted by mouse hepatic sinusoidal endothelial cells:
 RT identification as complement component C3b";
 RL Cancer Res. 53:4418-4423(1993).
 RN [7]
 RP ALTERNATIVE INITIATION
 RX MEDLINE=95053742; PubMed=7964485;
 RA Cahen-Kramer Y., Martensson I.L., Melchers F.;
 RA "The structure of an alternate form of complement C3 that displays

RT costimulatory growth factor activity for B lymphocytes."; J. Exp. Med. 180:2079-2088(1994).
 RL
 CC -1- FUNCTION: C3 PLAYS A CENTRAL ROLE IN THE ACTIVATION OF THE
 CC COMPLEMENT SYSTEM. ITS PROCESSING BY C3 CONVERTASE IS THE CENTRAL
 CC REACTION IN BOTH CLASSICAL AND ALTERNATIVE COMPLEMENT PATHWAYS.
 CC AFTER ACTIVATION C3B CAN BIND COVALENTLY, VIA ITS REACTIVE
 CC THIOESTER, TO CELL SURFACE CARBOHYDRATES OR IMMUNE AGGREGATES.
 CC -1- FUNCTION: DERIVED FROM PROTEOLYTIC DEGRADATION OF COMPLEMENT C3,
 CC C3A ANAPHYLATOXIN IS A MEDIATOR OF LOCAL INFLAMMATORY PROCESS. IT
 CC INDUCES THE CONTRACTION OF SMOOTH MUSCLE, INCREASES VASCULAR
 CC PERMEABILITY AND CAUSES HISTAMINE RELEASE FROM MAST CELLS AND
 CC BASOPHILIC LEUKOCYTES.
 CC -1- SUBUNIT: C3 PRECURSOR IS FIRST PROCESSED BY THE REMOVAL OF 4 ARG
 CC RESIDUES, FORMING TWO CHAINS, BETA & ALPHA, LINKED BY A DISULFIDE
 CC BOND. C3 CONVERTASE ACTIVATES C3 BY CLEAVING THE ALPHA CHAIN,
 CC RELEASING C3A ANAPHYLATOXIN & GENERATING C3B (BETA CHAIN + ALPHA
 CC CHAIN).
 CC -1- ALTERNATIVE PRODUCTS: A SHORT FORM IS PRODUCED BY THE USE OF AN
 CC ALTERNATIVE INITIATION CODON. THIS SHORT CHAIN HAS B-CELL
 CC STIMULATORY ACTIVITY.
 CC -1- MISCELLANEOUS: C3B IS RAPIDLY SPLIT IN TWO POSITIONS BY FACTOR I
 CC AND A COFACTOR TO FORM IC3B (INACTIVATED C3B) AND C3F WHICH IS
 CC RELEASED.
 CC -1- MISCELLANEOUS: IC3B IS THE SLOWLY CLEAVED (POSSIBLY BY FACTOR I)
 CC TO FORM C3C AND C3DG. OTHER PROTEASES PRODUCE OTHER FRAGMENTS SUCH
 CC AS C3D OR C3G.
 CC -1- SIMILARITY: TO C4, C5 AND ALPHA-2-MACROGLOBULIN.
 CC -1- SIMILARITY: CONTAINS 1 ANAPHYLATOXIN-LIKE DOMAIN.
 CC -----
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 CC -----
 DR EMBL; K02782; AAC42013.1; -;
 DR EMBL; J00369; AAA37336.1; -;
 DR EMBL; J00367; AAA37336.1; JOINED.
 DR EMBL; M33032; AAA37378.1; -;
 DR EMBL; Z37998; CAA86099.2; -;
 DR PIR; A05290; C3MS.
 DR HSSP; P01024; IC3D.
 DR MGD; MGI:88227; C3.
 DR InterPro; IPR002890; A2M_N.
 DR InterPro; IPR001599; Alpha_2_macroglbln.
 DR InterPro; IPR000020; Anaphylatoxin.
 DR InterPro; IPR001840; Anaphylatoxn.
 DR InterPro; IPR001134; Netrin_C.
 DR Pfam; PF00207; A2M; 1.
 DR Pfam; PF01835; A2M_N; 1.
 DR Pfam; PF01821; ANATO; 1.
 DR Pfam; PF01759; NTR; 1.
 DR PRINTS; PR00004; ANAPHYLATOXN.
 DR ProDom; PD003264; Anaphylatoxin; 1.
 DR SMART; SM00104; ANATO; 1.
 DR PROSITE; PS00477; ALPHA_2_MACROGLOBULIN; 1.
 DR PROSITE; PS01177; ANAPHYLATOXIN_1; 1.
 DR PROSITE; PS01178; ANAPHYLATOXIN_2; 1.
 DR Complement pathway; Complement alternate pathway; Plasma;
 KW Inflammatory response; Glycoprotein; Signal; Alternative initiation.
 FT SIGNAL 1 24
 FT CHAIN 25 1663 COMPLEMENT C3.
 FT CHAIN 25 666 COMPLEMENT C3, BETA CHAIN.
 FT CHAIN 671 1663 COMPLEMENT C3, ALPHA CHAIN.
 FT CHAIN 1129 1663 COMPLEMENT C3, SHORT ISOFORM.
 FT INIT_MET 1129 1129 FOR SHORT ISOFORM.
 FT PEPTIDE 671 748 C3A ANAPHYLATOXIN.
 FT CHAIN 749 1663 C3B (ALPHA' CHAIN).
 FT PEPTIDE 749 954 C3C FRAGMENT.
 FT PEPTIDE 955 1303 C3DG FRAGMENT.
 FT PEPTIDE 955 1001 C3G FRAGMENT.

RT and determination of their full-length cDNA sequences.";

RL An. J. Vet. Res. 59:704-711(1998).
 CC -1- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
 CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
 CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
 CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
 CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
 CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNIOVIAL CELLS
 CC (BY SIMILARITY).
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -1- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
 CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
 CC -1- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
 CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
 CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
 CC SECRETORY PROTEINS.
 CC -1- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; D42146; BAA07717.1; .
 CC EMBL; U92480; AAC39255.1; .
 CC HSP; P01583; LITA.
 CC InterPro: IPR002348; ILL_HBGF.
 CC InterPro: IPR000975; Interleukin_1.
 CC InterPro: IPR003502; Interleukin_1_prop.
 CC Pfam: PF00340; IL1; 1.
 CC Pfam: PF02394; IL1_propep; 1.
 CC PRINTS: PR00262; ILLHBGF.
 CC SMART: SM00125; IL1; 1.
 CC PROSITE: PS00253; INTERLEUKIN_1; 1.
 CC Cytokine: Macrophage; Mitogen; Inflammatory response; Pyrogen.
 CC PROPEP 1 112 BY SIMILARITY.
 CC CHAIN 113 270 INTERLEUKIN-1 ALPHA.
 CC CARBOHYD 141 141 N-LINKED (GLCNAC. .) (POTENTIAL).
 CC CONFLICT 110 110 R -> K (IN REF. 2).
 CC CONFLICT 150 150 G -> V (IN REF. 2).
 CC SEQUENCE 270 AA; 30806 MW; 381859713754DB90 CRC64;

Query Match .9.5%; Score 77.5; DB 1; Length 270;

Best Local Similarity 22.3%; Pred. No. 3.4; Mismatches 29; Conservative 29; Indels 11; Gaps 4;

QY 7 SKLSVIRNLNDQVLFIDQGNRPLFEDMTSDSCRONAPRTI-----FTISMYKDSQPRGMA 61
 Db 122 TKNFMRIHVHOCTLNDALNQSVIRDTSGOYLATAALNNLDDAVKFDMDGAYTSEDSQLP 181
 QY 62 VTSIV-KCEIKISTLSCENKIISKEM-NPPDNITKDKSDIIFQTSRVPGHDKMKQFESS 119
 Db 182 VTLRISKTRLFVSAQNEDEPVLLKEMPDPKTKIKDETNNLLFWER----HGSKNYKFSVA 237

QY 120 YEGYFLACEK 129

Db 238 HPKLFIATKQ 247

RESULT 13

OASB_MOUSE
 ID OASB_MOUSE STANDARD; PRT; 192 AA.
 AC Q60836;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 2'-5'-oligoadenylate synthetase 1B (EC 2.7.7.-) ((2'-5')jolligo(A)
 DE synthetase 1b) (2-5A synthetase 1B) (Fragment).
 GN OAS1B OR OIAS2.

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=91232962; PubMed=1709495;
 RA Rutherford M.N., Kumar A., Nissim A., Chebath J., Williams B.R.G.;
 RT "The murine 2-5A synthetase locus: three distinct transcripts from two
 RT linked genes";
 RL Nucleic Acids Res. 19:1917-1924(1991).
 CC -1- FUNCTION: THE 2-5A SYSTEM (THE OAS, 2-5A, AND RNASE L) MAY PLAY A
 CC ROLE IN MEDIATING RESISTANCE TO VIRUS INFECTION, CONTROL OF CELL
 CC GROWTH, DIFFERENTIATION, AND APOPTOSIS.
 CC -1- CATALYTIC ACTIVITY: BINDS DOUBLE-STRANDED RNA AND POLYMERIZES ATP
 CC INTO PPP(A2')P5'A/N OLIGOMERS, WHICH ACTIVATE THE LATENT RNASE L
 CC THAT, WHEN ACTIVATED, CLEAVES SINGLE-STRANDED RNAs.
 CC -1- INDUCTION: BY INTERFERONS.
 CC -1- SIMILARITY: BELONGS TO THE 2-5A SYNTHETASE FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; X55982; CAA39455.1; .
 CC MGD; MGI:97430; Oas1b.
 CC InterPro: IPR001797; 25A_synth.
 CC InterPro: IPR001201; PAP_25A_core.
 CC PROSITE: PS00832; 25A_SYNTH_1; PARTIAL.
 CC PROSITE: PS00833; 25A_SYNTH_2; PARTIAL.
 CC PROSITE: PS0152; 25A_SYNTH_3; 1.
 CC RNA-binding; Transferase; Nucleotidyltransferase;
 CC Interferon induction.
 CC NON_TER 1 1
 CC NON_TER 192 192
 CC SEQUENCE 192 AA; 21936 MW; 4E1C011EF9024F46 CRC64;

Query Match 9.3%; Score 75.5; DB 1; Length 192;

Best Local Similarity 23.2%; Pred. No. 3.5; Mismatches 42; Conservative 24; Indels 65; Gaps 9;

QY 3 GKLESKLSVIRN-----LNDQVLFIDQGNRPLFEDMTSDSCRONAPRTIISMYKD 54

Db 11 GRSDADLVFELNLTSTFEDLNQNGVLIKEIKQLCEVQHERRC----- 54

QY 55 SQPRGMAVTSVRKCEIKISTLSCENKIISKEMNPPONIKDKTSDII----- 100

Db 55 -----GVKFEVHSLRSPNSRALSFK-LSNPOLLKEVKFDVLPAYDLDDLHLNLKK 103

QY 101 -----FTQF-----SVP-GHDKMKQFESSYEGYFLACE--KERDLFKLI-----LKKDELG 145

Db 104 PNQOFYANLISGVPAKGKGLKICFMGLQKYLNCNRPDKLRLRLVTHWYQLCKE-KLG 162

QY 146 D 146

Db 163 D 163

RESULT 14

M3K8_MOUSE
 ID M3K8_MOUSE STANDARD; PRT; 467 AA.
 AC Q07174;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Mitogen-activated protein kinase kinase 8 (EC 2.7.1.-) (COT
 DE proto-oncogene serine/threonine-protein kinase) (C-COT) (Cancer osaka
 DE thyroid oncogene).


```

GN MAP3K8 OR COT.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=C57BL/6 x CBA; TISSUE=Thymus;
RC MEDLINE=93308016; PubMed=8320169;
RX Ohara R., Miyoshi J., Aoki M., Toyoshima K.;
RY "The murine cot proto-oncogene: genome structure and tissue-specific
RT expression.";
RT Jpn. J. Cancer Res. 84:518-525(1993).
RL -|- FUNCTION: Able to activate NF-kappa-B 1 by stimulating proteasome-
CC mediated proteolysis of NF-kappa-B 1/p105. Play a role in the cell
CC cycle (By similarity).
CC -|- SUBUNIT: Interacts with NFKB1/p105.
CC -|- SUBCELLULAR LOCATION: Cytoplasmic.
CC -|- TISSUE SPECIFICITY: High in adult submandibular gland, thymus,
CC spleen and newborn digestive tract.
CC -|- PTM: Autophosphorylated (By similarity).
CC -|- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC MAP KINASE KINASE SUBFAMILY.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to licenses@isb-sib.ch).
CC -----
DR EMBL: D13759; BAA02905.1; -
DR HSSP: Q00534; 1B18
DR MGD: MGI:1346878; Map3k8.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR Pfam: PF00069; pkinase; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR Transferase: Serine/threonine-protein kinase; Proto-oncogene;
KW ATP-binding; Phosphorylation.
FT DOMAIN 138 388 PROTEIN KINASE.
FT NP_BIND 144 152 ATP (BY SIMILARITY).
FT BINDING 167 167 ATP (BY SIMILARITY).
FT ACT_SITE 253 253 BY SIMILARITY.
FT SEQUENCE 467 AA; 52941 MW; 60C2A34E530866BE CRC64;
Query Match 9.2%; Score 75; DB 1; Length 467;
Best Local Similarity 24.0%; Pred. No. 11;
Matches 29; Conservative 22; Mismatches 36; Indels 34; Gaps 6;
Oy 12 IRLNDQVLFIDGGRNPLFDMDSDCRDNAPRTIFISMVKDSQPRGMATVISVKCEKI 71
| | | : | : | | : | | : | | : | | : | | : |
Db 361 MRLEIAALERNPNRPKAADLLKHEAL-NPPR-----EDQPR-----CQSL 401
Oy 72 STLSCEKN-IISKEMPPNNIKDT-----KSIDIFFORSVPGHDKMKQPFSSSTGY 123
| : | | : | : | : | : | : | : | : | : | : | : |
Db 402 DSALFERKLLSRKELQLPENIADSSCTGSTSESVLRQRS-----LYIDL GALAGY 454
Oy 124 F 124
Db 455 F 455
RESULT 15
RF1_TREPA STANDARD; PRT; 351 AA.
AC O83090;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)

```

GenCore version 4.5
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OM protein - protein search, using sw model
Run on: October 8, 2002, 10:16:41 ; Search time 43.19 seconds
(without alignments)
628.854 Million cell updates/sec

Title: SEQ6THRAT73
Perfect score: 816
Sequence: 1 YFGKLESLSVIRNLNDQVL.....LKKEDLGDRSIMFTVQNE 157

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 562222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL19:
1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mhc:
8: sp_organelle:
9: sp_phase:
10: sp_plant:
11: sp_rodent:
12: sp_virus:
13: sp Vertebrate:
14: sp Unclassified:
15: sp_rvirus:
16: sp_bacteriap:
17: sp_archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result		Query		Description	
No.	Score	Match	Length	ID	
1	803	98.4	193	4 Q96KJ8	Q96KJ8 homo sapien
2	797	97.7	193	6 Q9BG15	Q9BG15 macaca mula
3	659	80.8	178	6 Q9MZL8	Q9MZL8 bos taurus
4	653	80.0	193	6 Q9GL09	Q9GL09 ovis aries
5	639	78.3	192	6 Q95M33	Q95M33 felis silve
6	631	77.3	192	6 Q9N1P7	Q9N1P7 sus scrofa
7	446	54.7	196	11 Q91Z66	Q91Z66 sigmodon hi
8	318	39.0	84	6 Q95LE7	Q95LE7 canis famil
9	204	25.0	45	4 Q9NQ49	Q9NQ49 homo sapien
10	192	23.5	211	13 Q98SQ1	Q98SQ1 anas platyr
11	181.5	22.2	198	13 Q918D2	Q918D2 gallus gall
12	88	10.8	4643	5 Q9VW71	Q9VW71 drosophila
13	85	10.4	381	3 Q43031	Q43031 schizosacch
14	81.5	10.0	617	5 Q25986	Q25986 plasmodium
15	81.5	10.0	1049	2 Q93KF0	Q93KF0 caldicellul
16	81	9.9	263	3 Q74316	Q74316 schizosacch

17	80.5	9.9	866	16	O84500	chlamydia t
18	80	9.8	2470	13	Q90681	gallus gall
19	79.5	9.7	1044	3	Q94173	pneumocysti
20	79	9.7	452	16	O25249	helicobacte
21	78.5	9.6	204	2	Q92NJ7	clostridium
22	78.5	9.6	595	10	Q9SDM4	dunaliella
23	78	9.6	473	5	O16673	caenorhabdi
24	77.5	9.5	454	6	Q9BGD1	micronycter
25	77.5	9.5	840	12	Q9QBA2	yaba monkey
26	77.5	9.5	1251	13	Q91365	coturnix co
27	77	9.4	364	16	Q9PM33	campylobact
28	77	9.4	847	4	Q9NUC1	homo sapien
29	76.5	9.4	425	5	P90990	caenorhabdi
30	76.5	9.4	454	6	Q9BGA8	sturnira li
31	76	9.3	632	10	O80569	arabidopsis
32	76	9.3	747	10	O82393	arabidopsis
33	75.5	9.3	454	6	Q9BGE4	erophyllia s
34	75.5	9.3	454	6	Q9BGB7	phyllotomu
35	75.5	9.3	578	16	Q9PPR7	ureaplasma
36	75	9.2	445	13	O57610	scyllorhinu
37	75	9.2	1064	13	Q90601	gallus gall
38	75	9.2	1247	5	Q95QV2	caenorhabdi
39	74.5	9.1	137	5	O77077	plasmodium
40	74.5	9.1	334	10	Q9ZSB9	arabidopsis
41	74.5	9.1	454	6	Q9BGB8	phyllonycte
42	74.5	9.1	454	6	Q9BGB1	saccolaryx
43	74.5	9.1	974	11	Q924W2	rattus norv
44	74.5	9.1	1510	5	Q22699	caenorhabdi
45	74	9.1	245	17	Q97UG0	sulfolobus

ALIGNMENTS

RESULT 1

ID Q96KJ8 PRELIMINARY; PRT; 193 AA.
AC Q96KJ8;
DT 01-DEC-2001 (TREMREL. 19, Created)
DT 01-DEC-2001 (TREMREL. 19, Last sequence update)
DT 01-DEC-2001 (TREMREL. 19, Last annotation update)
DE INTERLEUKIN 18.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ying P., Jianxin L.;
RT "Cloning of Mutant Human Interleukin 18 cDNA";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF380360; AAK57024.1; ...
SQ SEQUENCE 193 AA; 22323 MW; 2E500205D1B7E5F7 CRC64;

Query Match	98.4%	Score 803;	DB 4;	Length 193;
Best Local Similarity	98.1%	Pred. No. 2.9e-73;		
Matches 154;	Conservative 2;	Mismatches 1;	Indels 0;	Gaps 0;
Qy 1	YFGKLESLSVIRNLNDQVLFDQGNRPLFEDMTDSCRDNAPRTIFIIISMYKDSQPRGM	60		
Db 37	YFGKLESLSVIRNLNNQVLFDQGNRPLFEDMTDSCRDNAPRTIFIIISMYKDSQPRGM	96		
Qy 61	AVTISVKEKISTLSCEKNKISFKEMNPPDNITKDKTSOIIFFQRSVPGHDKNMQFESSY	120		
Db 97	AVTISVKEKISTLSCEKNKISFKEMNPPDNITKDKTSOIIFFQRSVPGHDKNMQFESSY	156		
Qy 121	EGYFLACKEKRDLFLLKKEDELGDRSMTFTVQNE 157			
Db 157	EGYFLTCKEKRDLFLLKKEDELGDRSMTFTVQNE 193			
RESULT 2				

```

Q9BG15
ID Q9BG15 PRELIMINARY; PRT; 193 AA.
AC Q9BG15;
DT 01-JUN-2001 (TEMBLrel. 17, Created)
DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TEMBLrel. 17, Last annotation update)
DE INTERLEUKIN-18.
GN IL18.
OS Eucacia mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21229850; PubMed=11331040;
RA Glavetoni L.D., Imhoof J.D., Parodi L.M., Velasquillo C.M.,
RA Hodara V.L.;
RT "Expression of the Interleukin-18 Gene from Rhesus Macaque by the
RT Simian Immunodeficiency Virus Does Not Result In Increased Viral
RT Replication.";
RL J. Interferon, Cytokine Res. 21:173-180(2001).
DR EMBL; AF303732; AK13416.1; -.
SQ SEQUENCE 193 AA; 23225 MW; B2BD29C033BB0B5E CRC64;

Query Match 97.7%; Score 797; DB 6; Length 193;
Best Local Similarity 96.2%; Pred. No. 1.2e-72;
Matches 151; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSCDRNAPRTIFIISMYKDSQPRGM 60
DB 37 YFGKLESKLSIRNLNDQVLFIDQGNRPLFEDMTDSCDRNAPRTIFIINMYKDSQPRGM 96
QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIDKTSDIIFQFORSVPGHDKNQFESSY 120
DB 97 AVAISVKCEKISLSCENKIISFKEMNPPDNIDKTSDIIFQFORSVPGHDKNQFESSY 156
QY 121 EGYFLACEKERDLFKLILKKEDELGRSINFTVQNE 157
DB 157 EGYFLACEKERDLFKLILKKEDELGRSINFTVQNE 193

Query Match 80.8%; Score 659; DB 6; Length 178;
Best Local Similarity 78.3%; Pred. No. 3.9e-58;
Matches 123; Conservative 20; Mismatches 14; Indels 0; Gaps 0;

RESULT 3
Q9MZL8
ID Q9MZL8 PRELIMINARY; PRT; 178 AA.
AC Q9MZL8;
DT 01-OCT-2000 (TEMBLrel. 15, Created)
DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TEMBLrel. 17, Last annotation update)
DE INTERLEUKIN-18 (FRAGMENT).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=KIDNEY, LIVER, BLOOD MONONUCLEAR CELLS;
RA Olsen S.C., Lee I.K., Mwangi S.M., Kehrl M., Bolin C.A.;
RT "Cloning of bovine interleukin-18, expression in Escherichia coli, and
RT characterization of the biologic activities of the recombinant
RT cytokine.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF173175; AAF89833.1; -.
DR InterPro: IPR000975; Interleukin_1.
DR SMART: SM00125; IL1; 1.
FT NON_TER 178 178
FT SEQUENCE 178 AA; 20631 MW; 816D6B2B88ACB497 CRC64;

Query Match 80.8%; Score 659; DB 6; Length 178;

```

```

Best Local Similarity 77.7%; Pred. No. 8.9e-59;
Matches 122; Conservative 23; Mismatches 12; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSCDRNAPRTIFIISMYKDSQPRGM 60
DB 22 HFGLKLPKLSIRNLNDQVLFIDQGNRPLFEDMTDSCDRNAPRTIFIISMYKDSLTRGL 81
QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIDKTSDIIFQFORSVPGHDKNQFESSY 120
DB 82 AVTISVQCKMSTLSCENKIISFKEMNPPDNIDNEESDIIFQFORSVPGHDKIQFESSLY 141
QY 121 EGYFLACEKERDLFKLILKKEDELGRSINFTVQNE 157
DB 142 KGYFLACKKENDLFKLILKQDDNRDKSVNFTVQNON 178

RESULT 4
Q9GL09
ID Q9GL09 PRELIMINARY; PRT; 193 AA.
AC Q9GL09;
DT 01-MAR-2001 (TEMBLrel. 16, Created)
DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TEMBLrel. 17, Last annotation update)
DE INTERLEUKIN-18 (IGIF).
GN IL-18.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RA Bailey S.L., Gossner A., Dalziel R., Hopkins J.;
RT "Cloning of Ovine Interleukin 18 cDNA";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ401033; CAC09326.2; -.
DR InterPro: IPR000975; Interleukin_1.
DR SMART: SM00125; IL1; 1.
SQ SEQUENCE 193 AA; 22166 MW; CCDOA329062EF18C CRC64;

Query Match 80.0%; Score 653; DB 6; Length 193;
Best Local Similarity 78.3%; Pred. No. 3.9e-58;
Matches 123; Conservative 20; Mismatches 14; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSCDRNAPRTIFIISMYKDSQPRGM 60
DB 37 HFGLKLPKLSIRNLNDQVLFISQGNQPVFEDMPDSCDRNAPRTIFIISMYKDSLTRGL 96
QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIDKTSDIIFQFORSVPGHDKNQFESSY 120
DB 97 AVTISVQCKMSTLSCENKIISFKEMNPPDNIDNEESDIIFQFORSVPGHDKIQFESSLY 156
QY 121 EGYFLACEKERDLFKLILKKEDELGRSINFTVQNE 157
DB 157 KGYFLACKKENDLFKLILKQDDNRDKSVNFTVQNON 193

RESULT 5
Q9SM33
ID Q9SM33 PRELIMINARY; PRT; 192 AA.
AC Q9SM33;
DT 01-DEC-2001 (TEMBLrel. 19, Created)
DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
DE INTERFERON-GAMMA INDUCING FACTOR.
GN IGIF.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.

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```
Q9NQ49
ID Q9NQ49 PRELIMINARY; PRT; 45 AA.
AC Q9NQ49
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE INTERLEUKIN-18 (FRAGMENT).
GN IL-18.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Farhan A.J., Pravica V., Hutchinson I.V.;
RT "Identification of Human Interleukin-18 gene polymorphisms.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ295724; CAC01436.1; -
FT NON_TER 1 45
FT NON_TER 45 45
SQ SEQUENCE 45 AA; 5266 MW; DF3A626507E3D61A CRC64;

Query Match 25.0%; Score 204; DB 4; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.4e-13;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFDIOGGRPLFEDMTDSDCR 39
Db 7 YFGKLESKLSVIRNLNDQVLFDIOGGRPLFEDMTDSDCR 45

RESULT 10
Q98SQ1
ID Q98SQ1 PRELIMINARY; PRT; 211 AA.
AC Q98SQ1
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 18, Last sequence update)
DE INTERLEUKIN-18 (FRAGMENT).
GN IL-18.
OS Anas platyrhynchos (Domestic duck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
OX NCBI_TaxID=8839;
RN [1]
RP SEQUENCE FROM N.A.
RA Chan W.-S., Warr G.W., Middleton D.L., Lundquist M.L., Higgins D.A.;
RT "Anas platyrhynchos T-cell antigens, IL-18 gene.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF336122; AAK26322.1; -
DR InterPro; IPR000975; Interleukin_1.
DR SMART; SM00125; IL1; 1.
FT NON_TER 1 1
FT NON_TER 1 1
SQ SEQUENCE 211 AA; 24541 MW; CA6FC63538211B2B CRC64;

Query Match 23.5%; Score 192; DB 13; Length 211;
Best Local Similarity 36.5%; Pred. No. 1.4e-11;
Matches 61; Conservative 29; Mismatches 63; Indels 14; Gaps 9;

QY 2 FGKLESKLSVIRNLNDQVLFDIOG-NRPLFEDMTDSDCRNAPRTIFIISMYKDSQP-RG 59
Db 43 FSKEKTLHRLNRVNSQVLRVLPDLNVAAFEDVTDQEKSGSGMN-FCMHCYKTTTPSAG 101

QY 60 MAVTISVKCE-KISTLSCENK-----IISFKEMNPPDNKDKSDIIFQSRVPGHDNK-M 113
Db 102 MPVAFSRVEDKSYMCCEEHGKMIVRFREGEVPKDIPG-ESNIIFPKTFTSYSSKAF 160

QY 114 QFESSSYEGVFLACEKRDLFKLILKK---EDELGDRS-IMFTVQNE 156
Db 161 KFEYSLGRGFLAFEEEDSLRKLILKLPREDEVDETTKITLTSHNE 207
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RESULT 11
Q918D2
ID Q918D2 PRELIMINARY; PRT; 198 AA.
AC Q918D2
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE INTERLEUKIN 18.
GN IL-18.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Schneider K., Puehler F., Baeuerle D., Elvers S., Staeheli P.,
RA Kaspers B., Weining K.C.;
RT "cDNA cloning of biologically active chicken Interleukin-18.";
RL J. Interferon Cytokine Res. 20:879-883(2000).
DR EMBL; AJ277865; CAB96214.1; -
FT CHAIN 30 198 INTERLEUKIN 18.
FT CHAIN 30 198
SQ SEQUENCE 198 AA; 22918 MW; 29BB77DC3E3C6600 CRC64;

Query Match 22.2%; Score 181.5; DB 13; Length 198;
Best Local Similarity 36.8%; Pred. No. 1.4e-10;
Matches 57; Conservative 25; Mismatches 60; Indels 13; Gaps 7;

QY 13 RNLDQVLFDIOG-NRPLFEDMTDSDCRNAPRTIFIISMYKDSQP-RGMAVTISVKCEK 70
Db 42 RNVNSQLLVVLPDLNVAAFEDVTDQEVKSGS-GMYFDHCYKTTAPSGMPVAFSVQVED 100

QY 71 ISTLSCENK-----IISFKEMNPPDNKDKSDIIFQSRVPGHDNK-MQFESSSYEGYF 124
Db 101 KSYVMCEKEHGKMIVRFREGEVPKDIPG-ESNIIFPKTFTSCSKAFKFEYSLEQGMF 159

QY 125 LACEKERDLEKILKK---EDELGDRS-IMFTVQNE 156
Db 160 LAFEEDSLRKLILKLPREDEVDETTKFVTSHNE 194

RESULT 12
Q9VW71
ID Q9VW71 PRELIMINARY; PRT; 4643 AA.
AC Q9VW71
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE PUTATIVE FAT-LIKE CADHERIN PRECURSOR (CG7749 PROTEIN).
GN CG7749.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortman J.R., Fandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt J.G., Nelson C.R., Miklos G.L.G.,
RA Abrial J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
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RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
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RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Wellenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
CC -|- FUNCTION: MAY BE INVOLVED IN CELL ADHESION.
CC -|- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (POTENTIAL).
CC -|- SIMILARITY: BELONGS TO THE CADHERIN FAMILY.
CC -|- SIMILARITY: CONTAINS 5 EGF-LIKE DOMAINS.
CC -|- SIMILARITY: CONTAINS 1 LAMININ G-LIKE DOMAIN.
DR EMBL: AE003515; AAF49078.1; -;
DR HSP: P15116; 1NC1
DR FlyBase: FBgn0036930; fat2.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR002126; Cadherin.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR001791; Laminin_G.
DR Pfam: PF00028; cadherin; 33.
DR Pfam: PF00008; EGF; 5.
DR Pfam: PF00054; laminin_G; 1.
DR PRINTS: PS00205; CADHERIN.
DR SMART: SM00112; CA; 33.
DR SMART: SM00179; EGF_CA; 1.
DR SMART: SM00001; EGF_Like; 5.
DR SMART: SM00282; LamG; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; 1.
DR PROSITE: PS00232; CADHERIN_1; 1.
DR PROSITE: PS02368; CADHERIN_2; 41.
DR PROSITE: PS00022; EGF_1; 5.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01187; EGF_CA; 1.
KW Hypothetical protein; Cell adhesion; Signal; Transmembrane; Repeat;
KW EGF-like domain; Glycoprotein; Calcium-binding.
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FT DOMAIN 36 1647
FT TRANSMEM 1648 1668
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4643 AA; 517614 MW; 7EC5BD36ADD4E89 CRC64;
SQ SEQUENCE 4643 AA; 517614 MW; 7EC5BD36ADD4E89 CRC64;
Query Match 10.8%; Score 88; DB 5; Length 4643;
Best Local Similarity 23.6%; Pred. No. 15;
Matches 38; Conservative 25; Mismatches 56; Indels 42; Gaps 7;
QY 32 DMTSDSDCRNAPRTIFITSMY----KDSQPRGMVATISVKCEKISLSCENKIISF--KE 85
DB 2124 DISVLVDVNDNCP--LFVNMPYYATVSIDDPKG---TIIMQVKAIIDSDAENGVEYELKK 2178
QY 86 MNPPDNIKDKTSIIFFQSVFPHDNKMQFESSSVGYFLACEKRDL-----133
DB 2179 GNGELFKLDKSGELSIKHQVGHNRNRYELTVAAYDGAITPCSSSEAPLQVKVIDRMPVF 2238
QY 134 ---FKLILKKED-----ELGDRSIMFTVONE 156
DB 2239 EKQFTVSVKEDVEMYALSLSVIEAESPILG-RSLIYTTISSE 2278

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RESULT 13
O43031
ID O43031 PRELIMINARY; PRT; 381 AA.
AC O43031; Q9US93;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE HYPOTHETICAL 44.2 KDA PROTEIN C3B9.02C IN CHROMOSOME II.
GN SPC3B9.02C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RA Wood V., Rajandream M.A., Barrell B.G., Skelton J., Churcher C.M.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 140-321 FROM N.A.
RC STRAIN=968 H90;
RA Ding D.;
RT "Generation and analysis of GFP-gene fusion library of fission
  yeast.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -i- SIMILARITY: TO C.ELEGANS R11A8.2.
DR EMBL; AL022070; CAA17782.1; -.
DR EMBL; AB027944; BAA87248.1; -.
DR InterPro; IPR000467; G_patch.
DR SMART; SM00443; G_patch; 1.
KW Hypothetical protein.
SQ SEQUENCE 381 AA; 44214 MW; E1542538B667549F CRC64;

Query Match 10.4%; Score 85; DB 3; Length 381;
Best Local Similarity 26.4%; Pred. No. 1.7;
Matches 39; Conservative 23; Mismatches 54; Indels 32; Gaps 7;

QY 3 GKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTFIISMYKDSQPRGMV 62
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  ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DQ 208 GQLSSKQAF--DVNQRPTEFLGMGAKPYDSELTDLINWPKTKTF----- 250

QY 63 TISVK-CEKISTLSCENKIISF-KEMNPPDNKDKDIIFQSVPGHDKMKOFESSY 120
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DQ 251 -LPVKPLESALNSQNEHTVQKKSINL--TPSSSELFRRKS---RONNLSRESS-- 302

QY 121 EGYFLACEKERDLFKLILKKEDELGDLS 148
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DQ 303 -----VSSKHLDYNSRYNKRDRPDRT 325

RESULT 14
Q25986
ID Q25986 PRELIMINARY; PRT; 617 AA.
AC Q25986;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ORF PROTEIN (FRAGMENT).
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97098608; PubMed=8943148;
RA Bourke P.F., Holt D.C., Sutherland C.J., Kemp K.J.;
RT "Disruption of a Novel Open Reading Frame of P. Falciparum chromosome
  9 by Subtelomeric and Internal deletions Can Lead to Loss or
  Maintenance of Cytoadherence.";
RL Mol. Biochem. Parasitol. 82:25-36(1996).
DR EMBL; X95373; CAA64660.1; -.

Query Match 10.0%; Score 81.5; DB 2; Length 1049;
Best Local Similarity 21.8%; Pred. No. 12;
Matches 43; Conservative 26; Mismatches 61; Indels 67; Gaps 8;

QY 9 LSVIRNLNDQVLFIDQGNR-----PLFEDMTSDCRDNAPRTFIISMYKD 54
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DQ 635 LSTWELLEDGIIVDEGELDINLEPHCTAEVTPFRKELNLSCEYH----INIISLKS 690

QY 55 SQP----RGMAVT-----ISVCKEIKISLSCENKIISFKEMNPPDNKDKDIIFQSV 106
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  | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | :
DQ 691 STPWAKKGETVAVSQPRIPSKVAK-----KIINVNSLSQNLNKLKDENEIIVF--- 738

QY 107 PGHDNKKMFESS-----SYEGYFLACEK-----ERDLFKLIL 138
  | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
  | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DQ 739 -SEDTNVYFSKKRGTIINLYNNIELLKEGPSINLFRFTDNDKMKNTFFENDVFKLID 797

QY 139 KKEDELGDRSIMFTVQN 155
  : | : : : : |
DQ 798 AEEKVAFNELIISLAN 814
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Search completed: October 8, 2002, 10:16:42
Job time: 193 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 8, 2002, 10:14:17 ; Search time 20.63 seconds
(without alignments)
185.886 Million cell updates/sec

Title: SEQ6THRAT73

Perfect score: 816

Sequence: 1 YFGKLESKLSVIRNLNDQVL.....LAKKEDELGRSINFMTVQNE157

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 2442594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA.*

1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep.*

2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep.*

3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep.*

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6: /cgn2_6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	811	99.4	157	2	US-08-896-605A-6
2	811	99.4	157	2	US-08-896-501A-4
3	811	99.4	157	3	US-08-884-324-1
4	811	99.4	157	3	US-08-996-338-26
5	811	99.4	157	4	US-08-558-818-1
6	811	99.4	157	4	US-08-974-469A-1
7	811	99.4	157	4	US-08-832-180-1
8	811	99.4	157	4	US-08-832-198-6
9	811	99.4	193	2	US-08-896-605A-2
10	811	99.4	193	4	US-08-896-501A-2
11	811	99.4	193	4	US-08-832-180-9
12	518	63.5	157	2	US-08-502-535B-2
13	518	63.5	157	2	US-08-908-005A-2
14	518	63.5	157	3	US-08-996-338-27
15	518	63.5	157	4	US-08-558-818-7
16	518	63.5	157	4	US-08-974-469A-7
17	518	63.5	157	4	US-08-832-180-8
18	518	63.5	157	4	US-08-832-198-11
19	518	63.5	157	4	US-09-233-523-2
20	518	63.5	157	4	US-09-251-911-2
21	259	31.7	50	4	US-08-832-198-2
22	96	11.8	25	4	US-08-558-818-4
23	96	11.8	25	4	US-08-974-469A-4
24	96	11.8	25	4	US-08-832-180-4
25	96	11.8	25	4	US-08-832-198-8
26	90	11.0	17	4	US-08-832-198-5
27	81	9.9	155	6	5494663-8

28	81	9.9	267	6	5494663-5	Patent No. 5494663
29	77.5	9.5	270	2	US-08-611-880-1	Sequence 1, Appl
30	77.5	9.5	270	4	US-09-085-305-13	Sequence 13, Appl
31	75.5	9.3	270	4	US-09-085-305-20	Sequence 20, Appl
32	74	9.1	270	4	US-09-085-305-14	Sequence 14, Appl
33	73.5	9.0	855	2	US-08-482-090-12	Sequence 12, Appl
34	73.5	9.0	856	2	US-08-481-700B-8	Sequence 8, Appl
35	73.5	9.0	856	2	US-09-007-383-16	Sequence 16, Appl
36	72.5	8.9	268	4	US-09-085-305-8	Sequence 8, Appl
37	72.5	8.9	268	4	US-09-085-305-18	Sequence 18, Appl
38	72.5	8.9	1294	2	US-08-819-288-3	Sequence 3, Appl
39	72.5	8.9	1294	4	US-09-400-348-3	Sequence 3, Appl
40	72.5	8.9	1321	1	US-08-261-822A-3	Sequence 3, Appl
41	72.5	8.9	1321	5	PCT-US95-07744A-3	Sequence 3, Appl
42	71.5	8.8	268	4	US-09-085-305-10	Sequence 10, Appl
43	71.5	8.8	3418	3	US-08-755-587-44	Sequence 44, Appl
44	71	8.7	14	4	US-08-832-198-4	Sequence 4, Appl
45	71	8.7	1588	5	PCT-US93-07261-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-08-896-605A-6
; Sequence 6, Application US/08896605A
; Patent No. 5879942
; GENERAL INFORMATION:
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PROCESSING ENZYME FOR POLYPEPTIDE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/896.605A
; FILING DATE: 18 July 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 207.691/1996
; FILING DATE: 19-JUL-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 156.062/1997
; FILING DATE: 30-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: TANIMOTO-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-896-605A-6

Query Match 99.4%; Score 811; DB 2; Length 157;
Best Local Similarity 99.4%; Pred. No. 5.4e-88;
Matches 156; Conservative 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSCDRNAPRTIFIISMYKDSQPRGM 60
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Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSCDRNAPRTIFIISMYKDSQPRGM 60
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QY 61 AVTISVKCEKISLSCENKIISFKENPPDNIDKTSDIIFQSVPGHDKMKQFESSY 120
|||||
Db 61 AVTISVKCEKISLSCENKIISFKENPPDNIDKTSDIIFQSVPGHDKMKQFESSY 120
|||||
QY 121 EGYFLACERDLFKLILKEDELGDRSIMFTVQNE 157
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Db 121 EGYFLACERDLFKLILKEDELGDRSIMFTVQNE 157
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RESULT 2
US-08-896-501A-4
; Sequence 4, Application US/08896501A
; Patent No. 5891663
; GENERAL INFORMATION:
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PROCESS FOR PRODUCING POLYPEPTIDE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/896,501A
; FILING DATE: 18-JUL-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 213,267/1996
; FILING DATE: 25-JUL-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 31,474/1997
; FILING DATE: 31-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: TANIMOTO-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-896-501A-4

Query Match 99.4%; Score 811; DB 2; Length 157;
Best Local Similarity 99.4%; Pred. No. 5.4e-88;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSCDRNAPRTIFIISMYKDSQPRGM 60
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Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSCDRNAPRTIFIISMYKDSQPRGM 60
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QY 61 AVTISVKCEKISLSCENKIISFKENPPDNIDKTSDIIFQSVPGHDKMKQFESSY 120
|||||
Db 61 AVTISVKCEKISLSCENKIISFKENPPDNIDKTSDIIFQSVPGHDKMKQFESSY 120
|||||

QY 121 EGYFLACERDLFKLILKEDELGDRSIMFTVQNE 157
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Db 121 EGYFLACERDLFKLILKEDELGDRSIMFTVQNE 157
|||||
RESULT 3
US-08-884-324-1
; Sequence 1, Application US/08884324
; Patent No. 6060283
; GENERAL INFORMATION:
; APPLICANT: Takanori OKURA
; APPLICANT: Kakuji TORIGOE
; APPLICANT: Masahi KURIMOTO
; TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE
; OF INDUCING THE PRODUCTION OF INTERFERON-
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/884,324
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 185,305/96
; FILING DATE: 27-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: OKURA-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-884-324-1
Query Match 99.4%; Score 811; DB 3; Length 157;
Best Local Similarity 99.4%; Pred. No. 5.4e-88;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSCDRNAPRTIFIISMYKDSQPRGM 60
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Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSCDRNAPRTIFIISMYKDSQPRGM 60
|||||
QY 61 AVTISVKCEKISLSCENKIISFKENPPDNIDKTSDIIFQSVPGHDKMKQFESSY 120
|||||
Db 61 AVTISVKCEKISLSCENKIISFKENPPDNIDKTSDIIFQSVPGHDKMKQFESSY 120
|||||
QY 121 EGYFLACERDLFKLILKEDELGDRSIMFTVQNE 157
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Db 121 EGYFLACERDLFKLILKEDELGDRSIMFTVQNE 157
|||||
RESULT 4
US-08-996-338-26
; Sequence 26, Application US/08996338
; Patent No. 6087116
; GENERAL INFORMATION:

APPLICANT: TORIGOE, Kakuji
APPLICANT: OKURA, Takanori
TITLE OF INVENTION: KURIMOTO, Masashi
TITLE OF INVENTION: POLYPEPTIDES
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996.338
FILING DATE: 22-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 74,697/1997
FILING DATE: 12-MAR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 215,488/1997
FILING DATE: 28-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 291,837/1997
FILING DATE: 09-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TORIGOE-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 157
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-996-338-26

Query Match 99.4%; Score 811; DB 3; Length 157;
Best Local Similarity 99.4%; Pred. No. 5.4e-88;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 YFGKLESLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
Db 1 YFGKLESLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
Qy 61 AVTISVKEKISTLSCENKIISFKEMNPPDNKDKTSIIFFQRSVPGHDKNMQFESSY 120
Db 61 AVTISVKEKISTLSCENKIISFKEMNPPDNKDKTSIIFFQRSVPGHDKNMQFESSY 120
Qy 121 EGYFLACEKERDLFLKILKKEDELGDRSIMFTVQNEED 157
Db 121 EGYFLACEKERDLFLKILKKEDELGDRSIMFTVQNEED 157

RESULT 5
US-08-558-818-1
Sequence 1, Application US/08558818
Patent No. 6197297
GENERAL INFORMATION:
APPLICANT:
APPLICANT: NAME: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU
APPLICANT: KENKYUJO
APPLICANT: KUNITAKA, Toshio
APPLICANT: TANIGUCHI, Mutsuko
APPLICANT: KOHNO, Keizo

APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC TO POLYPEPTIDE
TITLE OF INVENTION: WHICH INDUCES INTERFERON- PRODUCTION
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W. Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect Version 5.0
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: FELICI-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/558.818
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: JP 58,240/95
PRIOR APPLICATION DATA: February 23, 1995
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 157 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-558-818-1

Query Match 99.4%; Score 811; DB 4; Length 157;
Best Local Similarity 99.4%; Pred. No. 5.4e-88;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 YFGKLESLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
Db 1 YFGKLESLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
Qy 61 AVTISVKEKISTLSCENKIISFKEMNPPDNKDKTSIIFFQRSVPGHDKNMQFESSY 120
Db 61 AVTISVKEKISTLSCENKIISFKEMNPPDNKDKTSIIFFQRSVPGHDKNMQFESSY 120
Qy 121 EGYFLACEKERDLFLKILKKEDELGDRSIMFTVQNEED 157
Db 121 EGYFLACEKERDLFLKILKKEDELGDRSIMFTVQNEED 157

RESULT 6
US-08-974-469A-1
Sequence 1, Application US/08974469A
Patent No. 6207641
GENERAL INFORMATION:
APPLICANT: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU
APPLICANT: KENKYUJO
APPLICANT: TORIGOE, Kakuji
APPLICANT: TANIMOTO, Tadao
APPLICANT: FUKUDA, Shigeharu
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: AGENT FOR SUSCEPTIVE DISEASE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W. Ste. 300
CITY: Washington

STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect Version 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,469A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/599,879
FILING DATE:
APPLICATION NUMBER: JP 78,357/95
FILING DATE: March 10, 1995
APPLICATION NUMBER: JP 274,988/95
FILING DATE: September 29, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TORIGOB-1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 157 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-974-469A-1

Query Match 99.4%; Score 811; DB 4; Length 157;
Best Local Similarity 99.4%; Pred. No. 5.4e-88;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 YFGKLESKLVIRNLNDQVLFIDQGNRPFLFEDMTDSDCRDNAPRTTIFIIISMYKDSQPRGM 60
DB 1 YFGKLESKLVIRNLNDQVLFIDQGNRPFLFEDMTDSDCRDNAPRTTIFIIISMYKDSQPRGM 60
QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIDKTSDIIFQFORSVPGHDKMKQFESSY 120
DB 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIDKTSDIIFQFORSVPGHDKMKQFESSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSINFTVQNE 157
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSINFTVQNE 157

RESULT 7
US-08-832-180-1
Sequence 1, Application US/08832180
Patent No. 6214584
GENERAL INFORMATION:
APPLICANT: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU
APPLICANT: KENYUJO
APPLICANT: USHIO, Shimpel
APPLICANT: TORIGOE, Kakuji
APPLICANT: TANIMOTO, Tadao
APPLICANT: OKAMURA, Haruki
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: POLYPEPTIDE PRODUCTION INDUCING
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W. Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA

ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect Version 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/832,180
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/558,191
FILING DATE:
APPLICATION NUMBER: JP 304,203/94
FILING DATE: No. 6214584ember 15, 1994
APPLICATION NUMBER: 10048102
FILING DATE: September 18, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: USHIO-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 157 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-832-180-1

Query Match 99.4%; Score 811; DB 4; Length 157;
Best Local Similarity 99.4%; Pred. No. 5.4e-88;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 YFGKLESKLVIRNLNDQVLFIDQGNRPFLFEDMTDSDCRDNAPRTTIFIIISMYKDSQPRGM 60
DB 1 YFGKLESKLVIRNLNDQVLFIDQGNRPFLFEDMTDSDCRDNAPRTTIFIIISMYKDSQPRGM 60
QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIDKTSDIIFQFORSVPGHDKMKQFESSY 120
DB 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIDKTSDIIFQFORSVPGHDKMKQFESSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSINFTVQNE 157
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSINFTVQNE 157

RESULT 8
US-08-832-198-6
Sequence 6, Application US/08832198
Patent No. 6242255
GENERAL INFORMATION:
APPLICANT: AKITA, Kenji
APPLICANT: NUKADA, Yoshiyuki
APPLICANT: FUJII, Mitsukiyo
APPLICANT: TANIMOTO, Tadao
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: PROTEIN WHICH INDUCES INTERLEUKIN-GAMMA
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/832,198
FILING DATE: 08-APR-1997
CLASSIFICATION: 51A
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/721,018
FILING DATE: 25-SEP-1996
APPLICATION NUMBER: JP 95-270725
FILING DATE: 26-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 96-067434
FILING DATE: 29-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP not yet received
FILING DATE: 20-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: AKITA-1
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 157 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
OTHER INFORMATION: "Xaa" in position 73 is either
OTHER INFORMATION: "Ile" or "Thr"

US-08-832-198-6

Query Match 99.4%; Score 811; DB 4; Length 157;
Best Local Similarity 99.4%; Pred. No. 5.4e-88;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
|||||
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
|||||

Qy 61 AVTISVCKEISTLSCEKNIISFKEMNPPDNKDTKSDIIFQFORSVFGHDKMKQFESSY 120
|||||
Db 61 AVTISVCKEISTLSCEKNIISFKEMNPPDNKDTKSDIIFQFORSVFGHDKMKQFESSY 120
|||||

Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
|||||
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
|||||

RESULT 9
US-08-896-605A-2
Sequence 2, Application US/08896605A
Patent No. 5879942
GENERAL INFORMATION:
APPLICANT: TANIMOTO, Tadao
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: PROCESSING ENZYME FOR POLYPEPTIDE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/896,605A
FILING DATE: 18 JULY 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 207,691/1996
FILING DATE: 19-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 156,062/1997
FILING DATE: 30-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TANIMOTO-2
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 193 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-896-605A-2

Query Match 99.4%; Score 811; DB 2; Length 193;
Best Local Similarity 99.4%; Pred. No. 7.2e-88;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
|||||
Db 37 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 96
|||||

Qy 61 AVTISVCKEISTLSCEKNIISFKEMNPPDNKDTKSDIIFQFORSVFGHDKMKQFESSY 120
|||||
Db 97 AVTISVCKEISTLSCEKNIISFKEMNPPDNKDTKSDIIFQFORSVFGHDKMKQFESSY 156
|||||

Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
|||||
Db 157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 193
|||||

RESULT 10
US-08-896-501A-2
Sequence 2, Application US/08896501A
Patent No. 5891663
GENERAL INFORMATION:
APPLICANT: TANIMOTO, Tadao
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: PROCESS FOR PRODUCING POLYPEPTIDE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/896,501A
FILING DATE: 18-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 213,267/1996
FILING DATE: 25-JUL-1996

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 31,474/1997
; FILING DATE: 31-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, ROGER L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: TANIMOTO-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 193 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-896-501A-2

Query Match 99.4%; Score 811; DB 2; Length 193;
Best Local Similarity 99.4%; Pred. No. 7.2e-88;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTFIFIISMYKDSQPRGM 60
|||||
DB 37 YFGKLESLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTFIFIISMYKDSQPRGM 96
QY 61 AVTISVKEKISTLSCENKIISFKEMNPPDNITKDSIIFFQRSVPGHNDKMQPESY 120
|||||
DB 97 AVTISVKEKISTLSCENKIISFKEMNPPDNITKDSIIFFQRSVPGHNDKMQPESY 156
QY 121 EGYFLACEKERDLFLILKKEDELGDRSIMFTVQNE 157
|||||
DB 157 EGYFLACEKERDLFLILKKEDELGDRSIMFTVQNE 193

RESULT 11
US-08-832-180-9

; Sequence 9, Application US/08832180
; Patent No. 6214584

; GENERAL INFORMATION:

; APPLICANT: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU

; APPLICANT: KENYUJO

; APPLICANT: USHIO, Shimpai

; APPLICANT: TORIGOE, Kakui

; APPLICANT: TANIMOTO, Tadao

; APPLICANT: OKAMURA, Haruki

; APPLICANT: KURIMOTO, Masashi

; TITLE OF INVENTION: INTERFERON- PRODUCTION INDUCING

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Browdy and Neimark

; STREET: 419 Seventh Street N.W. Ste. 300

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Word Perfect Version 5.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/832,180

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/558,191

; FILING DATE:

; APPLICATION NUMBER: JP 304,203/94

; FILING DATE: No. 6214584ember 15, 1994

; APPLICATION NUMBER: 10048102
; FILING DATE: September 18, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Browdy, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: USHIO-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 193 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-832-180-9

Query Match 99.4%; Score 811; DB 4; Length 193;
Best Local Similarity 99.4%; Pred. No. 7.2e-88;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTFIFIISMYKDSQPRGM 60
|||||
DB 37 YFGKLESLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTFIFIISMYKDSQPRGM 96
QY 61 AVTISVKEKISTLSCENKIISFKEMNPPDNITKDSIIFFQRSVPGHNDKMQPESY 120
|||||
DB 97 AVTISVKEKISTLSCENKIISFKEMNPPDNITKDSIIFFQRSVPGHNDKMQPESY 156
QY 121 EGYFLACEKERDLFLILKKEDELGDRSIMFTVQNE 157
|||||
DB 157 EGYFLACEKERDLFLILKKEDELGDRSIMFTVQNE 193

RESULT 12

US-08-502-535B-2

; Sequence 2, Application US/08502535B

; Patent No. 5912324

; GENERAL INFORMATION:

; APPLICANT: OKAMURA, Haruki

; APPLICANT: TANIMOTO, Tadao

; APPLICANT: TORIGOE, Kakui

; APPLICANT: KUNIKATA, Toshio

; APPLICANT: TANIGUCHI, Mutsuko

; APPLICANT: KOHNO, Keizo

; APPLICANT: KURIMOTO, Masashi

; TITLE OF INVENTION: IFN-BETA PRODUCTION INDUCING PROTEIN AND

; MONOCLONAL ANTIBODY OF THE SAME

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BROWDY AND NEIMARK

; STREET: 419 Seventh Street, N.W., Suite 300

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/502,535B

; FILING DATE: 14-JUL-1995

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 184162/1994

; FILING DATE: 14-JUL-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 45057/1995

; FILING DATE: 10-FEB-1995

ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: OKAMURA-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 157 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-502-535B-2

Query Match 63.5%; Score 518; DB 2; Length 157;
Best Local Similarity 65.6%; Pred. No. 1.8e-53;
Matches 101; Conservative 26; Mismatches 25; Indels 2; Gaps 2;
QY 2 FGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTDSDCRONAPRTIFITISMYKDSQPRGMA 61
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Db 2 FGLHCTTAVIRNINQVLFVDK-RQPVFEDMTDIDQSASEPQTRLIYMYKDSVVRGLA 60
||:| :|||:|||||:| :|:||||| :|:| |||:||||| :||:
QY 62 VTISVCKEISTLSCENKIISFKEMNPPDNKDKSDIIFQSRVPGHDKMKMFESSYE 121
||:| :|||:|||||:| :|:||||| :|:| |||:||||| :||:
Db 61 VTLSVKDSKXSTLSCKNKIISFEEMDPDENIDDIQSDLIFFQKRVPGH-NKMEFESSLYE 119
||:| :|||:|||||:| :|:||||| :|:| |||:||||| :||:
QY 122 GYFLACEKERDLFKLILKKKEDELGDRSIMFTVQN 155
||:| :|||:|||||:| :|:||||| :|:| |||:||||| :||:
Db 120 GHFLACQKEDDAFLKILKKKDKGSKVSMFTLTN 153
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RESULT 13
US-08-908-005A-2
Sequence 2, Application US/08908005A
Patent No. 5914253
GENERAL INFORMATION:
APPLICANT: OKAMURA, Haruki
APPLICANT: TANIMOTO, Tadao
APPLICANT: TORIGOE, Kakuji
APPLICANT: KUNIKATA, Toshio
APPLICANT: TANIGUCHI, Mutsuko
APPLICANT: KOHNO, Keizo
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: IFN-BETA PRODUCTION INDUCING PROTEIN AND
TITLE OF INVENTION: MONOCLONAL ANTIBODY OF THE SAME
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NETMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/908,005A
FILING DATE: 11-AUG-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/502,535
FILING DATE: 14-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 184162/1994
FILING DATE: 14-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 45057/1995
FILING DATE: 10-FEB-1995

ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: OKAMURA-2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 157 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-908-005A-2
Query Match 63.5%; Score 518; DB 2; Length 157;
Best Local Similarity 65.6%; Pred. No. 1.8e-53;
Matches 101; Conservative 26; Mismatches 25; Indels 2; Gaps 2;
QY 2 FGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTDSDCRONAPRTIFITISMYKDSQPRGMA 61
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Db 2 FGLHCTTAVIRNINQVLFVDK-RQPVFEDMTDIDQSASEPQTRLIYMYKDSVVRGLA 60
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QY 62 VTISVCKEISTLSCENKIISFKEMNPPDNKDKSDIIFQSRVPGHDKMKMFESSYE 121
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Db 61 VTLSVKDSKXSTLSCKNKIISFEEMDPDENIDDIQSDLIFFQKRVPGH-NKMEFESSLYE 119
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QY 122 GYFLACEKERDLFKLILKKKEDELGDRSIMFTVQN 155
||:| :|||:|||||:| :|:||||| :|:| |||:||||| :||:
Db 120 GHFLACQKEDDAFLKILKKKDKGSKVSMFTLTN 153
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RESULT 14
US-08-996-338-27
Sequence 27, Application US/08996338
Patent No. 6087116
GENERAL INFORMATION:
APPLICANT: TORIGOE, Kakuji
APPLICANT: OKURA, Takahori
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: POLYPEPTIDES
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NETMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,338
FILING DATE: 22-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 74,697/1997
FILING DATE: 12-MAR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 215,488/1997
FILING DATE: 28-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 291,837/1997
FILING DATE: 09-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TORIGOE-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197

; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-996-338-27

Query Match 63.5%; Score 518; DB 3; Length 157;
Best Local Similarity 65.6%; Pred. No. 1.8e-53;
Matches 101; Conservative 26; Mismatches 25; Indels 2; Gaps 2;
Qy 2 FQKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMVKDSOPRGMA 61
Db 2 FQRLHCTTAVIRNINDQVLFVDK-RQPVFEDMTDIDQASASEPQTRLIIYMYKDSVRGLA 60
Qy 62 VTISVKCEKISLSCENKIISFKEMNPPDNINKDTSKDIFFQRSVPGHDNKNMFESSSVE 121
Db 61 VTLSVKDSKXSTLSCNKKIISFEEMDPDENIDDIQSDLIFFQKRVPGH-NKMEFESSLYE 119
Qy 122 GYFLACERDLFKLILKKEDELGRSIMFTVON 155
Db 120 GHFLACQEDDAFKLILKKEDEGDKSVNFTLTN 153

RESULT 15
US-08-558-818-7
; Sequence 7, Application US/08558818
; Patent No. 6197297
; GENERAL INFORMATION:
; APPLICANT: NAME: KARUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU
; APPLICANT: KENYUJO
; APPLICANT: KUNIKATA, Toshio
; APPLICANT: TANIGUCHI, Mutsuko
; APPLICANT: KOHNO, Keizo
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC TO POLYPEPTIDE
; TITLE OF INVENTION: WHICH INDUCES INTERFERON- PRODUCTION
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street N.W. Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect Version 5.0
; ATTORNEY/AGENT INFORMATION:
; NAME: Browdy, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: FELICI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/558,818
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: JP 58,240/95
; PRIOR APPLICATION DATA: February 23, 1995
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: mouse
; INDIVIDUAL ISOLATE: liver
US-08-558-818-7
Query Match 63.5%; Score 518; DB 4; Length 157;
Best Local Similarity 65.6%; Pred. No. 1.8e-53;
Matches 101; Conservative 26; Mismatches 25; Indels 2; Gaps 2;
Qy 2 FQKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMVKDSOPRGMA 61
Db 2 FQRLHCTTAVIRNINDQVLFVDK-RQPVFEDMTDIDQASASEPQTRLIIYMYKDSVRGLA 60
Qy 62 VTISVKCEKISLSCENKIISFKEMNPPDNINKDTSKDIFFQRSVPGHDNKNMFESSSVE 121
Db 61 VTLSVKDSKXSTLSCNKKIISFEEMDPDENIDDIQSDLIFFQKRVPGH-NKMEFESSLYE 119
Qy 122 GYFLACERDLFKLILKKEDELGRSIMFTVON 155
Db 120 GHFLACQEDDAFKLILKKEDEGDKSVNFTLTN 153

Search completed: October 8, 2002, 10:14:18
Job time: 529 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 8, 2002, 10:10:39 ; Search time 51.43 Seconds
(without alignments)
339.074 Million cell updates/sec

Title: SEQ6ILEAT73

Perfect score: 815

Sequence: 1 YFGKLESLKSVIRNLNDQVL.....LKKEDELGRSIMEFTVQVNE 157

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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10: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1989.DAT.*
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19: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	810	99.4	157	17	AA99564 Human interferon-g
2	810	99.4	157	17	AA99558 Human mature inter
3	810	99.4	157	18	AAW15701 Interferon-gamma 1
4	810	99.4	157	18	AAW24258 Human protein for
5	810	99.4	157	19	AAW77158 Human interleukin-
6	810	99.4	157	19	AAW77077 Human interleukin
7	810	99.4	157	19	AAW63810 Human IL-18 protei
8	810	99.4	157	19	AAW37741 IFN-gamma inducing
9	810	99.4	157	19	AAW52176 Interferon-gamma 1
10	810	99.4	157	20	AAW39799 Interleukin-18 rec
11	810	99.4	157	21	AAW44597 Human interleukin-

12	810	99.4	157	21	AAW53904 Sequence of a matu
13	810	99.4	157	21	AAW57570 Human interleukin
14	810	99.4	157	22	AAE06661 Human interleukin-
15	810	99.4	157	22	AAW82408 Human interleukin-
16	810	99.4	157	22	AAW65294 Human interleukin-
17	810	99.4	157	22	AAW65351 Human interleukin-
18	810	99.4	158	21	AAW85167 Human interleukin-
19	810	99.4	180	19	AAW48959 Wild-type human in
20	810	99.4	193	17	AAW99560 Human interferon-g
21	810	99.4	193	18	AAW22047 Interferon-gamma 1
22	810	99.4	193	19	AAW37740 Interferon-gamma 1
23	810	99.4	193	19	AAW52172 Interferon-gamma 1
24	810	99.4	193	19	AAW47429 Interferon-gamma p
25	810	99.4	193	19	AAW46592 Amino acid sequenc
26	810	99.4	193	21	AAW53908 Amino acid sequenc
27	810	99.4	193	22	AAW82409 Human interleukin-
28	810	99.4	193	22	AAW30541 Human IL-18 with
29	810	99.4	193	22	AAW63830 Amino acid sequenc
30	807	99.0	193	19	AAW77082 Interleukin 18 act
31	802	98.4	193	18	AAW31757 Interferon gamma 1
32	800	98.2	157	19	AAW77083 Human interleukin
33	800	98.2	157	19	AAW48961 Mutant human inter
34	800	98.2	181	21	AAW23797 Human interleukin
35	791	97.1	193	22	AAW72608 Macaca cynomolgus
36	790	96.9	157	19	AAW77084 Human interleukin
37	790	96.9	157	19	AAW77085 Human interleukin
38	790	96.9	157	19	AAW48962 Mutant human inter
39	790	96.9	157	19	AAW48963 Mutant human inter
40	781	95.8	157	19	AAW77080 Human interleukin
41	781	95.8	157	19	AAW77088 Human interleukin
42	781	95.8	157	19	AAW48966 Mutant human inter
43	780	95.7	157	19	AAW77086 Human interleukin
44	780	95.7	157	19	AAW48964 Mutant human inter
45	771	94.6	157	19	AAW77081 Human interleukin

ALIGNMENTS

RESULT	1
AA99564	AA99564 standard; Protein; 157 AA.
ID	AC
XX	AA99564;
XX	AC
XX	29-SEP-1996 (first entry)
DT	XX
DE	Human interferon-gamma inducer protein.
XX	XX
XX	Interferon-gamma inducer protein; IFN-gamma; antiviral; virucide;
KW	antitumour; antibacterial; immunoregulator; adoptive immunotherapy;
KW	therapy; cancer.
XX	XX
OS	Homo sapiens.
XX	XX
FH	Key Location/Qualifiers
FT	Misc-difference 73
FT	/label= Ile, Thr
XX	XX
PN	EP712931-A2.
XX	XX
PD	22-MAY-1996.
XX	XX
PF	10-NOV-1995; 95EP-0308055.
XX	XX
PR	29-SEP-1995; 95JP-0274988.
PR	15-NOV-1994; 94JP-0304203.
PR	23-FEB-1995; 95JP-0058240.
PR	10-MAR-1995; 95JP-0078357.
PR	18-SEP-1995; 95JP-0262062.
XX	XX
XX	(HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
XX	XX

XX 20-SEP-1996; 96JP-0269105.
 PR 26-SEP-1995; 95JP-0270725.
 PR 29-FEB-1996; 96JP-0067434.
 XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 PI Akita K, Fujii M, Kurimoto M, Nukada Y, Tanimoto T;
 XX WPI; 1997-205381/19.
 DR Human protein that induces interferon-gamma prodn. in
 XX immuno:competent cells - useful for adoptive immuno:therapy of
 PT tumours and as antimicrobial agent etc.
 PT Claim 8; Page 20; 26pp; English.
 PS The present sequence represents a novel protein from human cells, which
 XX induces interferon-gamma (IFN gamma) production in immunocompetent cells.
 CC This protein enhances cytotoxicity of killer cells and induces their
 CC formation. It is used as an antineoplastic agent for antitumour
 CC immunotherapy. an antiviral (including anti-AIDS) or antibacterial agent,
 CC and in the treatment of atopic or immune system diseases, e.g. asthma,
 CC hayfever or rheumatism. When formulated with interleukin-3, it is also
 CC used to treat leukaemia and thrombocytopaenia associated with
 CC radiotherapy or chemotherapy of leukaemia and other cancers. When used in
 CC antitumour immunotherapy, this novel protein significantly improves the
 CC immunotherapeutic effect of interleukin-2 (IL-2), compared with use of
 CC IL-2 alone, either when administered to the patient (before
 CC administration of IL-2) or by addition to the medium in which cells
 CC (intended for return to the patient) are being grown.
 XX SQ Sequence 157 AA;

Query Match 99.4%; Score 810; DB 18; Length 157;
 Best Local Similarity 99.4%; Pred. No. 8.1e-83;
 Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60
 DB 1 Yfgklesklsvirnlndqvlfidqgnrplfedmtsdcrdnaprtifiismvkdsqprgm 60
 QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDTSKDIFFQRSVPGHDKMKQFESSY 120
 DB 61 avtisvkcekislscenkliisfkemppdnikdtskdiiffqrsvpgdhdkmqfessy 120
 QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
 DB 121 egyflacekerdlfkilkkedelgdrsifmftvqned 157

RESULT 4
 AAW24258
 ID AAW24258 standard; Protein; 157 AA.
 XX AAW24258;
 XX 15-OCT-1997 (first entry)
 DT Human protein for induction of interferon-gamma.
 DE Interferon-gamma; immunocompetent cell; malignant tumour;
 KW viral disease; bacterial infection; immune disease.
 XX Homo sapiens.
 OS Key Location/Qualifiers
 FH Misc-difference 73
 FT /note= "Encoded by AYT"
 XX JP09157180-A.

PD 17-JUN-1997.
 XX 24-JAN-1996; 96JP-0028722.
 XX 04-OCT-1995; 95JP-0279906.
 PR 10-MAR-1995; 95JP-0078357.
 PR 29-SEP-1995; 95JP-0274988.
 XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 PA WPI; 1997-369391/34.
 DR N-PSDB; AAT80209.
 XX A drug containing a polypeptide which induces interferon-gamma -
 PT useful for treating e.g. malignant tumours, viral, bacterial or
 PT immune diseases
 PT Claim 1; Page 9; 12pp; Japanese.
 PS This sequence represents a protein which induces Interferon-gamma
 XX production in immunocompetent cells. This protein may be used as
 CC the major component in a drug for the prevention and treatment of
 CC e.g. malignant tumours, viral diseases, bacterial infections and
 CC immune diseases.
 XX SQ Sequence 157 AA;

Query Match 99.4%; Score 810; DB 18; Length 157;
 Best Local Similarity 99.4%; Pred. No. 8.1e-83;
 Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60
 DB 1 Yfgklesklsvirnlndqvlfidqgnrplfedmtsdcrdnaprtifiismvkdsqprgm 60
 QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDTSKDIFFQRSVPGHDKMKQFESSY 120
 DB 61 avtisvkcekislscenkliisfkemppdnikdtskdiiffqrsvpgdhdkmqfessy 120
 QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
 DB 121 egyflacekerdlfkilkkedelgdrsifmftvqned 157

RESULT 5
 AAW77158
 ID AAW77158 standard; Protein; 157 AA.
 XX AAW77158;
 XX 26-NOV-1998 (first entry)
 DT Human interleukin-18 protein (IL-18).
 DE Human; interleukin-18 receptor; IL-18R; cytokine; signal transduction;
 KW immune system; treatment; autoimmune; allergic disease;
 KW immunosuppressant.
 XX Homo sapiens.
 OS Key Location/Qualifiers
 FH Misc-difference 73
 FT /note= "Ile or Thr"
 XX EP864585-A1.
 PD 16-SEP-1998.
 XX 23-DEC-1997; 97EP-0310517.
 PR 09-OCT-1997; 97JP-0291837.
 PR 12-MAR-1997; 97JP-0074697.

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PR 28-JUL-1997; 97JP-0215488.
XX (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
XX
XX Kurimoto M, Okura T, Torigoe K;
XX
XX WPI; 1998-469188/41.
XX
XX Interleukin-18 receptor polypeptide(s) - and corresponding DNA,
XX which peptide compounds are useful for treating auto-immune or
XX allergic diseases
XX
XX Disclosure: Pages 41-42; 51pp; English.
XX
XX The present sequence represents a human interleukin-18 (IL-18)
XX polypeptide. Interleukin-18 is a type of cytokine which mediates signal
XX transduction in immune systems. The interleukin-18 receptor polypeptide
XX can be used to neutralise interleukin-18 activity or to treat
XX Interleukin-18 receptor susceptible diseases, especially to treat
XX auto-immune or allergic diseases or as an immunosuppressant. Conditions
XX which may be treated include e.g. graft or organ rejection, pernicious
XX anaemia, insulin-related diabetes, discoid lupus erythematosus,
XX ulcerative colitis, hyperthyroidism, auto-immune hepatitis, systemic
XX scleroderma, polymyositis, leukopenia, rheumatoid arthritis, HIV
XX infections, asthma, atopic dermatitis, and pollinosis. The products may
XX also be useful in the treatment of septic shock associated with
XX IFN-alpha.
XX
XX Sequence 157 AA;
SQ

```

Query Match 99.4%; Score 810; DB 19; Length 157;
Best Local Similarity 99.4%; Pred. No. 8.1e-83;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSCRDNAPRTIFIISMYKDSQPRGM 60
DB 1 yfgklesklsvirnlndqvlfidqgnrplfedmtsdscrdnaprtifiismykdsgprgm 60
QY 61 AVTISVCKEISILSCENKIISFKEMNPPDNIKDTKSDIIFQFORSVPGHDKMKQFESSY 120
DB 61 avtisvckekisilscenkliisfkemppdnikatsdiiffqrsvpghdnkmqfessy 120
QY 121 EGYFLACEKERDLFKLILKKREDELGDRSIMFTVQNE 157
DB 121 egyflacekerdlfkllkkedeldgdrsimftvqned 157

```

RESULT 6
AAW77077
ID AAW77077 standard; peptide; 157 AA.
XX
XX AAW77077;
XX
XX 16-NOV-1998 (first entry)
XX
XX Human interleukin 18.
XX
XX Human; interleukin-18; IL-18; osteoclast; hypercalcaemia; osteopenia;
XX osteoclastoma Behcet's syndrome; osteosarcoma; arthropathy; osteoporosis;
XX chronic rheumatoid arthritis; deformity ostitis; primary hyperthyroidism.
XX
XX Homo sapiens.
XX
XX EP861663-A2.
XX
XX 02-SEP-1998.
XX
XX 24-FEB-1998; 98EP-0301352.
XX
XX 25-FEB-1997; 97JP-0055468.
XX
XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

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XX Gillespie MT, Horwood NJ, Kurimoto M, Udagawa N;
XX
XX WPI; 1998-448964/39.
XX N-PSDB; AAV48226.
XX
XX Use of Interleukin-18 to inhibit osteoclast formation - in treatment
XX of e.g. hypercalcaemia, osteoclastoma, Behcet's syndrome,
XX osteosarcoma, chronic rheumatoid arthritis, deformity ostitis,
XX primary hyperthyroidism and osteoporosis
XX
XX Claim 4; Page 18; 56pp; English.
XX
XX Interleukin-18 (IL-18) or a functional equivalent can be used for
XX inhibition of osteoclast formation. IL-18 is used for treating or
XX preventing osteoclast-related diseases e.g. hypercalcaemia, osteoclastoma
XX Behcet's syndrome, osteosarcoma, arthropathy, chronic rheumatoid
XX arthritis, deformity ostitis, primary hyperthyroidism, osteopenia and
XX osteoporosis.
XX
XX Sequence 157 AA;
SQ

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Query Match 99.4%; Score 810; DB 19; Length 157;
Best Local Similarity 99.4%; Pred. No. 8.1e-83;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSCRDNAPRTIFIISMYKDSQPRGM 60
DB 1 yfgklesklsvirnlndqvlfidqgnrplfedmtsdscrdnaprtifiismykdsgprgm 60
QY 61 AVTISVCKEISILSCENKIISFKEMNPPDNIKDTKSDIIFQFORSVPGHDKMKQFESSY 120
DB 61 avtisvckekisilscenkliisfkemppdnikatsdiiffqrsvpghdnkmqfessy 120
QY 121 EGYFLACEKERDLFKLILKKREDELGDRSIMFTVQNE 157
DB 121 egyflacekerdlfkllkkedeldgdrsimftvqned 157

```

RESULT 7
AAW63810
ID AAW63810 standard; protein; 157 AA.
XX
XX AAW63810;
XX
XX 28-SEP-1998 (first entry)
XX
XX Human IL-18 protein fragment.
XX
XX Interleukin-18; IL-18; human; treatment; autoimmune disease; antibody;
XX immunosuppressant; inhibitor; receptor protein; detection.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Protein 1..157
XX /label= IL-18
XX /note= "partial sequence"
XX Misc-difference 73
XX /label= Thr or Ile
XX
XX EP850952-A1.
XX
XX 01-JUL-1998.
XX
XX 23-DEC-1997; 97EP-0310555.
XX
XX 28-JUL-1997; 97JP-0215490.
XX 26-DEC-1996; 96JP-0356426.
XX 21-FEB-1997; 97JP-0052526.
XX 06-JUN-1997; 97JP-0163490.
XX

PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 XX Kunikata T, Kurimoto M, Torigoe K, Ushio S;
 PI WPI: 1998-335317/30.
 XX
 XX New interleukin-18 receptor protein used to inhibit interleukin-18,
 PT to treat autoimmune disease and as immunosuppressant - and new
 PT monoclonal antibody and hybridoma used to detect interleukin -18
 PT receptor protein
 XX
 PS Claim 5; Page 16; 35pp; English.
 XX
 XX This sequence represents a human interleukin-18 (IL-18) fragment which is
 CC used in a method involved in neutralising IL-18 or to treat autoimmune
 CC diseases or as an immunosuppressant using anti-IL-18 antibodies which
 CC can inhibit IL-18. Such antibodies can also be used to detect the IL-18
 CC receptor protein (labelled with an enzyme or a radioactive or fluorescent
 CC substance). The protein is used to treat e.g. graft rejection, pernicious
 CC anaemia, atrophic gastritis, insulin-resistant diabetes, Wegener
 CC granulomatosis, discoid lupus erythematosus, ulcerative colitis,
 CC cold-agglutinin-related diseases, Goodpasture's syndrome, primary
 CC biliary cirrhosis, sympathetic ophthalmitis, hyperthyroidism, juvenile
 CC onset type diabetes, Sjogren syndrome, autoimmune hepatitis, autoimmune
 CC haemolytic anaemia, myasthenia gravis, systemic scleroderma, systemic
 CC lupus erythematosus, polytopic cold haemaglobinuria, polymyositis,
 CC periarthritis nodosa, multiple sclerosis, Addison's disease, purpura
 CC haemorrhagica, Basedow's disease, leukopaenia, Behcet's disease,
 CC Chlamydiae praecox, rheumatoid arthritis, rheumatopyria, chronic
 CC thyroiditis, Hodgkin's disease, HIV, asthma, atopic dermatitis, allergic
 CC nasitis, pollinosis, epitoxin-allergy and septic shock resulting from
 CC production or administration of excessive gamma interferon (IFN-gamma).
 XX
 XX Sequence 157 AA;

Query Match 99.4%; Score 810; DB 19; Length 157;
 Best Local Similarity 99.4%; Pred. No. 8.1e-83;
 Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTFIISMYKDSQPRGM 60
 DB 1 Yfgklesklsvirnlndqvlfidqgnrpflfedmtsdcrdnaprtfiismykdsqprgm 60
 QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDKTSIIFFQRSVPGHDNKMQFESSY 120
 DB 61 avtisvkcekisxlscenkliisfkemppdnikdtktsiiffqrsvpghdnkmqfessy 120
 QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
 DB 121 egyflacekerdlfkilkkedelgdrsImftvqned 157

RESULT 8
 AAW37741
 ID AAW37741 standard; Protein; 157 AA.
 XX
 AC AAW37741;
 XX
 DT 07-JUL-1998 (first entry)
 XX
 DE IFN-gamma inducing active protein.
 XX
 KW Interferon-gamma inducing precursor peptide; IFN-gamma;
 KW Interleukin-1-beta-converting enzyme; ICE; cytotoxicity; killer cell;
 KW antiviral agent; antitumour agent; immunopathy agent; antiseptic.
 XX
 OS Mammalia.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 73
 FT /label= Ile, Thr
 XX

PN EP821005-A2.
 XX
 PD 28-JAN-1998.
 XX
 PF 18-JUL-1997; 97EP-0305376.
 XX
 PR 31-JAN-1997; 97JP-0031474.
 PR 25-JUL-1996; 96JP-0213267.
 XX
 PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 XX
 PI Kurimoto M, Tanimoto T;
 XX
 DR WPI: 1998-088847/09.
 DR N-PSDB; AAV18906.
 XX
 PT Conversion of interferon-inducing polypeptide precursor to active
 PT polypeptide - comprises use of interferon-1-beta-converting enzyme,
 PT useful for, e.g. enhancing cytotoxicity by killer cells
 XX
 PS Claim 5; Page 15; 18pp; English.
 XX
 XX This is the amino acid sequence for the interferon-gamma (IFN-gamma)
 CC inducing active protein which is cleaved to form the active mature
 CC protein when it is in contact with interleukin-1-beta-converting
 CC enzyme (ICE). The polypeptide is used for inducing, e.g. production
 CC of IFN-gamma a useful biologically active substance, enhancing
 CC cytotoxicity by, and inducing the formation of killer cells. The
 CC polypeptide may potentially be used as an antiviral, antitumour and
 CC immunopathy agent and as an antiseptic.
 XX
 XX Sequence 157 AA;

Query Match 99.4%; Score 810; DB 19; Length 157;
 Best Local Similarity 99.4%; Pred. No. 8.1e-83;
 Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTFIISMYKDSQPRGM 60
 DB 1 Yfgklesklsvirnlndqvlfidqgnrpflfedmtsdcrdnaprtfiismykdsqprgm 60
 QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDKTSIIFFQRSVPGHDNKMQFESSY 120
 DB 61 avtisvkcekisxlscenkliisfkemppdnikdtktsiiffqrsvpghdnkmqfessy 120
 QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
 DB 121 egyflacekerdlfkilkkedelgdrsImftvqned 157

RESULT 9
 AAW52176
 ID AAW52176 standard; peptide; 157 AA.
 XX
 AC AAW52176;
 XX
 DT 10-JUN-1998 (first entry)
 XX
 DE Interferon-gamma inducing mature polypeptide.
 XX
 KW Interferon-gamma; IFN-gamma; precursor; enzyme; cleavage.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 73
 FT /label= Ile, Thr
 XX
 PN EP819757-A2.
 XX
 PD 21-JAN-1998.
 XX

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PF 18-JUL-1997; 97EP-0305377.
XX
PR 30-MAY-1997; 97JP-0156062.
PR 19-JUL-1996; 96JP-0207691.
XX
PA (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
XX
PI Kurimoto M, Tanimoto T;
XX
DR WPI; 1998-079838/08.
XX
PT Polypeptide-processing enzyme - for preparing mature form of
PT interferon-inducing polypeptide
XX
PS Claim 20; Page 17; 18pp; English.
XX
CC This is an Interferon-gamma (IFN-gamma) inducing polypeptide sequence.
CC This polypeptide induces IFN-gamma production in immunocompetent cells
CC [the polypeptide is not named but is described in JP 27198/96 and
CC 193098/96]. An enzyme can convert the precursor form of this polypeptide
CC into this active form by cleaving a linkage between Asp at amino acid
CC position 36 and Tyr at amino acid position 37 of the precursor. The
CC enzyme can be obtained from a human haematopoietic cell and can be
CC inhibited by iodoacetamide and acetyl-L-tyrosyl-L-valyl-L-alanyl-L-
CC aspart-1-al. The enzyme can be used for cleaving a recombinant IFN-gamma
CC pro-polypeptide to form a mature polypeptide.
XX
SQ Sequence 157 AA;

Query Match 99.4%; Score 810; DB 19; Length 157;
Best Local Similarity 99.4%; Pred. No. 8.le-83;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDGGRPLFEDMTSDCRDNAPRTIFIIISMYKDSQPRGM 60
Db 1 yfgklesklsvirnlndqvlfdggnrplfedmtsdcrdnaprtrifilismykdsgprgm 60

Qy 61 AVTISVCKEISILSCENKIISFKEMNPPDNKDKTSDIIFQSVPGHDNKMOPESSY 120
Db 61 avtislsvckeisilscenkiisfkemppdnkdktsdiiiffqsvpghdnkmqfessy 120

Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEQ 157
Db 121 egyflacekerdlfklikkedelgdrsimftvqned 157

RESULT 10
AAV39799
ID AAV39799 standard; Protein; 157 AA.
XX
AC AAV39799;
XX
DT 29-NOV-1999 (first entry)
XX
DE Interleukin-18 receptor protein sequence fragment.
XX
KW Interleukin-18 receptor; IL-18; human; mouse; organ transplant rejection;
KW IL-18 receptor sensitive disease; immune reaction; therapy.
XX
OS Mammalia.
XX
FH Key Location/Qualifiers
FT Misc-difference 73 /note= "unspecified amino acid"
FT
XX
PN JPI1240898-A.
XX
PD 07-SEP-1999.
XX
PF 12-MAR-1998; 98JP-0078549.
XX
PR 12-MAR-1997; 97JP-0074697.
XX

28-JUL-1997; 97JP-0215488.
PR 09-OCT-1997; 97JP-0291837.
PR 26-DEC-1997; 97JP-0366908.
XX
PA (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
XX
DR WPI; 1999-555071/47.
XX
PT New polypeptide - useful against interleukin-18 receptor sensitive
PT diseases
XX
PS Disclosure; Page 37; 41pp; Japanese.
XX
CC This sequence is a fragment of an interleukin-18 receptor (IL-18R) of the
CC invention. The IL-18R sequences were isolated from human and mouse. The
CC sequences can be used in drugs for treating IL-18 receptor sensitive
CC disease, especially effective for the relief of rejection accompanied to
CC organ transplantation and for the treatment and the prevention of various
CC diseases caused by excessive immune reaction.
XX
SQ Sequence 157 AA;

Query Match 99.4%; Score 810; DB 20; Length 157;
Best Local Similarity 99.4%; Pred. No. 8.le-83;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDGGRPLFEDMTSDCRDNAPRTIFIIISMYKDSQPRGM 60
Db 1 yfgklesklsvirnlndqvlfdggnrplfedmtsdcrdnaprtrifilismykdsgprgm 60

Qy 61 AVTISVCKEISILSCENKIISFKEMNPPDNKDKTSDIIFQSVPGHDNKMOPESSY 120
Db 61 avtislsvckeisilscenkiisfkemppdnkdktsdiiiffqsvpghdnkmqfessy 120

Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEQ 157
Db 121 egyflacekerdlfklikkedelgdrsimftvqned 157

RESULT 11
AAV44597
ID AAV44597 standard; Protein; 157 AA.
XX
AC AAV44597;
XX
DT 04-APR-2000 (first entry)
XX
DE Human interleukin-18.
XX
KW Human interleukin-18; IL-18; anti-IL-18-antibody; immunopathies;
KW inflammatory disorder; autoimmune disease; anti-allergic;
KW anti-inflammatory; immunosuppressive; hematopoietic; leukocytopoietic;
KW antialgic; antipyretic.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 73 /label= Ile, Thr
FT
XX
PN EP974600-A2.
XX
PD 26-JAN-2000.
XX
PF 24-JUN-1999; 99EP-0304977.
XX
PR 24-JUN-1998; 98JP-0177580.
PR 12-OCT-1998; 98JP-0289044.
PR 22-DEC-1998; 98JP-0365023.
XX
PA (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
XX

```

PI Nishida Y, Okura T, Tanimoto T, Kurimoto M;
DR WPI; 2000-118341/11.
XX
PT New artificially produced peptide for neutralizing biological activity
PT of interleukin-18, useful for treating and preventing immunopathies,
PT inflammatory disorders and autoimmune diseases -
XX
XX Example 1; Page 26; 32pp; English.
PS
XX The present sequence is human interleukin-18. This was used to immunise
CC BALB/c mice to generate hybridomas that produce anti-IL-18 antibodies for
CC neutralising interleukin-18. This is useful for treating and preventing
CC immunopathies, inflammatory disorders and autoimmune diseases which are
CC caused by excessive immunoreaction. The protein has anti-allergic
CC anti-inflammatory, immunosuppressive, hematopoietic, leukocytopoietic,
CC antiagtic, antipyretic and hepatic-function improving activities.
XX
SQ Sequence 157 AA;
Query Match 99.4%; Score 810; DB 21; Length 157;
Best Local Similarity 99.4%; Pred. No. 8.le-83;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFITSMYKDSQPRGM 60
Db 1 yfgklesklsvirnlndqvlfidqgnrplfedmtsdcrdnaprtrifiismykdsqprgm 60
Qy 61 AVTISVKEKISILSCENKIISFKEMNPPDNIKDTKSDIIFQRSVPGDHNMQFESSY 120
Db 61 avtisvkekisxlscenkiisfkemppdnikdtkdsliiffqrsvpghdnkmqfessy 120
Qy 121 EGYFLACEKERDLFLKLLKKEDELGDRSIMFTVQNEQ 157
Db 121 egyflacekerdlfklllkkedelgdrsimftvqned 157
RESULT 12
AAV53904
ID AAV53904 standard; Protein: 157 AA.
AC AAV53904;
DT 13-MAR-2000 (first entry)
XX
DE Sequence of a mature protein that induces IFN-gamma production.
KW Human; interferon gamma production; IFN-gamma; immunocompetent cell;
KW antiviral; immunoregulatory; antigen; mitogen;
KW IFN-gamma susceptible disease; antibacterial; antitumour;
KW blood platelet enhancing agent; hepatitis; herpes syndrome; condyloma;
KW AIDS; bacterial disease; candidiasis; malaria; solid malignant tumour;
KW renal cancer; mycosis fungoides; chronic granulomatous disease;
KW blood cell malignant tumour; adult T cell leukaemia;
KW chronic myelogenous leukaemia; malignant leukaemia; immune disease;
KW allergy; rheumatism.
XX
OS Homo sapiens.
FH
FT Key Location/Qualifiers
FT Misc-difference 73
FT /label= Ile, Thr
FT /note= "encoded by AYT"
PN EP962531-A2.
XX
PD 08-DEC-1999.
XX
PF 10-NOV-1995; 99EP-0104104.
XX
XX 15-NOV-1994; 94JP-0304203.
PR 23-FEB-1995; 95JP-0058240.
PR

PR 10-MAR-1995; 95JP-0078357.
PR 18-SEP-1995; 95JP-0262062.
PR 29-SEP-1995; 95JP-0274988.
PR 10-NOV-1995; 95EP-0308055.
XX
PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
XX
PI Ushio S, Torigoe K, Tanimoto T, Okamura H;
XX
XX WPI; 2000-064289/06.
DR N-PSDB; AAZ36875.
XX
PT Novel polypeptides used in the treatment of Interferon-gamma
PT susceptible diseases -
XX
XX Claim 1; Page 4; 42pp; English.
XX
CC The present sequence represnets a human protein that induces Interferon
CC (IFN)-gamma production by immunocompetent cells. IFN-gamma is a
CC protein which has antiviral, antioncotic and immunoregulatory activities,
CC and is produced by immunocompetent cells stimulated with antigens or
CC mitogens. The protein of the invention is used to treat IFN-gamma
CC susceptible diseases, and also have use as a antiviral agent,
CC antibacterial agent, antitumour agent, immunoregulatory agent and blood
CC platelet enhancing agent. Diseases which can be treated with the
CC protein include viral diseases such as hepatitis, herpes syndrome,
CC condyloma, and AIDS; bacterial diseases such as candidiasis and
CC malaria; solid malignant tumours such as renal cancer, mycosis
CC fungoides, and chronic granulomatous disease; blood cell malignant
CC tumours such as adult T cell leukaemia, chronic myelogenous leukaemia,
CC and malignant leukaemia; and immune diseases such as allergy and
CC rheumatism.
XX
SQ Sequence 157 AA;
Query Match 99.4%; Score 810; DB 21; Length 157;
Best Local Similarity 99.4%; Pred. No. 8.le-83;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFITSMYKDSQPRGM 60
Db 1 yfgklesklsvirnlndqvlfidqgnrplfedmtsdcrdnaprtrifiismykdsqprgm 60
Qy 61 AVTISVKEKISILSCENKIISFKEMNPPDNIKDTKSDIIFQRSVPGDHNMQFESSY 120
Db 61 avtisvkekisxlscenkiisfkemppdnikdtkdsliiffqrsvpghdnkmqfessy 120
Qy 121 EGYFLACEKERDLFLKLLKKEDELGDRSIMFTVQNEQ 157
Db 121 egyflacekerdlfklllkkedelgdrsimftvqned 157
RESULT 13
AAV57570
ID AAV57570 standard; protein; 157 AA.
XX
AC AAV57570;
XX
XX 06-MAR-2000 (first entry)
DT
XX Human interleukin 18 protein sequence SEQ ID NO:1.
DE
XX Human; interleukin 18; IL-18; potentlator; IGIF;tumour; cancer;
KW interferon-gamma-inducing factor; growth inhibition; cytostatic.
KW
XX Homo sapiens.
OS
XX WO9959565-A1.
PN
XX 25-NOV-1999.
PD
XX 20-MAY-1999; 99WO-US11160.
PF

```

XX 21-MAY-1998; 98US-0086560.
XX (SMIK ) SMITHKLINE BEECHAM CORP.
XX Johnson RK;
XX WPI; 2000-062368/05.
XX New polypeptides, useful for preparation of composition for preventing
XX and/or treating cancer by inhibiting tumor growth -
XX Claim 1; Page 49-50; 53pp; English.
XX The present sequence represents human interleukin 18 (IL-18). The
XX present invention describes a compound comprising human or murine IL-18
XX in combination with a chemotherapeutic agent (I). Also described are:
XX (1) a method of preventing and/or treating cancer in a mammal comprising
XX the administration of a cancer inhibiting amount of (I) comprising the
XX IL-18 protein and the chemotherapeutic agent and optionally a
XX pharmaceutically acceptable carrier; and (2) a method of inhibiting the
XX growth of tumour cells in a mammal sensitive to a composition comprising
XX human IL-18 and/or murine IL-18 and the chemotherapeutic agent (and
XX optionally a pharmaceutically acceptable carrier), comprising
XX administering to a mammal afflicted with the tumour cells an effective
XX tumour cell growth inhibiting amount of (I). The IL-18 protein in
XX conjunction with a chemotherapeutic agent is useful in a method for
XX preventing and/or treating cancer in mammals by inhibiting the growth
XX of tumours or cancerous cells in mammals.
XX Sequence 157 AA;

Query Match 99.4%; Score 810; DB 21; Length 157;
Best Local Similarity 99.4%; Pred. No. 8.1e-83;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSCRDNAPRTIFIISMYKDSQPRGM 60
DB 1 yfgklesklsvirnlndqvlfidqgnrplfedmtsdscrdnaprtifiismykdsgprgm 60

QY 61 AVTISVKCEKISILSCENKIISFKEMPPDNIDTKSDIIFFQFORSVPGHDKNQFESSY 120
DB 61 avtislsvkcekislscenkiiskfemppdnidktsdiiffqforsvpgdhknqmfessy 120

QY 121 EGYFLACEKERDLFKLILKKKEDELGDRSIMFTVQNE 157
DB 121 egyptlaccerdlfklllkkkedelgdrsimftvqned 157

RESULT 14
AAE06661
ID AAE06661 standard; Protein; 157 AA.
XX AAE06661;
XX 16-OCT-2001 (first entry)
XX Human interleukin-1gamma (IL-1gamma) protein.
XX Human; interleukin-1gamma; IL-1gamma; virucide; hepatotropic; fever;
XX immunological disorder; tumour; inflammatory disorder; hypoglycaemia;
XX autoimmune disease; pulmonary tuberculosis; fulminant hepatitis; leprosy;
XX psoriasis; viral infection; allergy; cytokine; HIV; drug screening.
XX Homo sapiens.
XX WO200157219-A2.
XX 09-AUG-2001.
XX 01-FEB-2001; 2001WO-US03285.
XX

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```

PR 02-FEB-2000; 2000US-0179638.
XX (SCHE ) SCHERING CORP.
XX Debets JEMA, Timans JC, Bazan JF, Kastelein RA;
XX WPI; 2001-488886/53.
XX Novel isolated or recombinant antigenic interleukin-1 delta or epsilon
XX polypeptide useful for treating conditions exhibiting abnormal
XX expression of interleukin such as immunological disorders, tumor and
XX allergy -
XX Disclosure; Fig 1; 103pp; English.
XX The invention relates to recombinant antigenic interleukin-1 like
XX molecules and their corresponding nucleic acid sequences, designated
XX as interleukin-1delta (IL-1delta) and interleukin-1epsilon (IL-1epsilon).
XX IL-1delta and IL-1epsilon are useful for treating conditions exhibiting
XX abnormal expression of the interleukin such as immunological disorders,
XX tumours, inflammatory disorders, fever, hypoglycaemia, psoriasis,
XX allergy, autoimmune diseases and infectious diseases (e.g., pulmonary
XX tuberculosis, leprosy, fulminant hepatitis, and viral infections such as
XX HIV). The invention also relates to methods of using the composition
XX containing IL-1delta or IL-1epsilon for both diagnostic and therapeutic
XX utilities. IL-1delta is used as an immunogen for the production of
XX antisera or antibodies specific, e.g., capable of distinguishing between
XX IL-1 family members and an IL-1delta, for the interleukin or its
XX fragment. The purified interleukin is used as a reagent to detect any
XX antibodies generated in response to the presence of elevated levels of
XX expression, or immunological disorders which lead to antibody production
XX to the endogenous cytokine. The invention also contemplates the use of
XX competitive drug screening assays. The present sequence is human
XX interleukin-1gamma (IL-1gamma) protein related to the invention.
XX Sequence 157 AA;

Query Match 99.4%; Score 810; DB 22; Length 157;
Best Local Similarity 99.4%; Pred. No. 8.1e-83;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSCRDNAPRTIFIISMYKDSQPRGM 60
DB 1 yfgklesklsvirnlndqvlfidqgnrplfedmtsdscrdnaprtifiismykdsgprgm 60

QY 61 AVTISVKCEKISILSCENKIISFKEMPPDNIDTKSDIIFFQFORSVPGHDKNQFESSY 120
DB 61 avtislsvkcekislscenkiiskfemppdnidktsdiiffqforsvpgdhknqmfessy 120

QY 121 EGYFLACEKERDLFKLILKKKEDELGDRSIMFTVQNE 157
DB 121 egyptlaccerdlfklllkkkedelgdrsimftvqned 157

RESULT 15
AAB82408
ID AAB82408 standard; Protein; 157 AA.
XX AAB82408;
XX 06-AUG-2001 (first entry)
XX Human interleukin-18 mature polypeptide.
XX Interleukin-18; antibody; human; infection; tumour; sarcoma;
XX autoimmune disease; therapy; diagnosis; detoxification.
XX Homo sapiens.
XX Key Location/Qualifiers
XX Misc-difference 73 /label= Ile, Thr
XX FT

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 8, 2002, 10:12:19 ; Search time 28.21 seconds
(without alignments)
534.776 Million cell updates/sec

Title: SEQ6ILEAT73

Perfect score: 815

Sequence: 1 YFGKLESKLSVIRNLNDQVL.....LKKDELGDRSIMFTVQNE 157

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_71.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	514	63.1	192	2 S60226	cytokine IGIF - mouse
2	84	10.3	381	2 T40341	hypothetical prote
3	84	10.3	452	2 D64583	hypothetical prote
4	83.5	10.2	270	1 S10532	interleukin-1 alph
5	83.5	10.2	866	2 C71509	probable DNA polym
6	82	10.1	263	2 T39487	hypothetical prote
7	82	10.1	364	2 A81261	probable periplasm
8	79	9.7	632	2 T00679	hypothetical prote
9	78.5	9.6	192	2 S15661	hypothetical prote
10	78	9.6	473	2 T32038	(2'-5')oligo(A) sy
11	77.5	9.5	270	2 I46620	hypothetical prote
12	77.5	9.5	1228	2 A57384	interleukin-1 alph
13	76.5	9.4	204	2 T44357	multimerin, endoth
14	76.5	9.4	1036	2 H64245	hypothetical prote
15	76	9.3	450	2 G71928	hypothetical prote
16	76	9.3	747	2 E84698	hypothetical prote
17	75.5	9.3	1251	2 A56677	neuronal cell cycl
18	75	9.2	354	2 E97128	magnesium and ciba
19	75	9.2	1738	2 T14867	interactin - slime
20	75	9.2	2663	1 S28261	centromere protein
21	74.5	9.1	268	1 B24073	interleukin-1 alph
22	74.5	9.1	334	2 T04198	hypothetical prote
23	74.5	9.1	888	2 A38539	pi01 protein precu
24	74.5	9.1	1663	1 C3MS	complement C3 prec
25	74	9.1	245	2 B90488	hypothetical prote
26	74	9.1	376	2 T24925	hypothetical prote
27	74	9.1	1064	1 S57450	protein-tyrosine k
28	74	9.1	2470	2 I50726	cation-independent
29	73.5	9.0	375	2 T29568	hypothetical prote

ALIGNMENTS

RESULT 1

S60226

cytokine IGIF - mouse

C:Species: Mus musculus (house mouse)

C:Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 20-Jun-2000

C:Accession: S60226

R:Okamura, H.; Tsutsui, H.; Komatsu, T.; Yutsudo, M.; Hakura, A.; Tanimoto, T.; Torig

Nature 378, 88-91, 1995

A:Title: Cloning of a new cytokine that induces IFN-gamma production by T cells.

A:Reference number: S60226; MUID:96061009

A:Accession: S60226

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-192 <OKA>

A:Cross-references: EMBL:D49949; NID:g1064822; PIDN:BAA08705.1; PID:g1064823

C:Superfamily: Mus musculus cytokine IGIF

Query Match 63.1%; Score 514; DB 2; Length 192;

Best Local Similarity 64.9%; Pred. No. 2.4e-41;

Matches 100; Conservative 27; Mismatches 25; Indels 2; Gaps 2;

Qy 2 FGKLESKLSVIRNLNDQVLFDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGMA 61

Db 37 FGLRHCTTAVIRNLNDQVLFDK-RQPVFEDMTDIDQSASEPQTRLIIIMYKDSVRLGA 95

Qy 62 VTISVKCEKISILSCENKIIISFKEMNPPDNIKDTKSDIIFFQSVPGHDNKMQFESSVE 121

Db 96 VTLSVKDSKMSLTSCNKKIISFEEMDPENIDDDIQSDLIFFQKRVPGH-NKMEFESSLYE 154

Qy 122 GYFLACERDLFKLILKKEDELGDRSIMFTVQN 155

Db 155 GHFLACQKEDDAFLKILKKDKENGSKSVMTLTN 188

RESULT 2

T40341

hypothetical protein SPBC3B9.02c - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999

C:Accession: T40341

R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M.

submitted to the EMBL Data Library, March 1997

A:Reference number: 221922

A:Accession: T40341

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-381 <WOO>

A:Cross-references: EMBL:AL022070; PIDN:CAA17782.1; GSPDB:GN00067; SPDB:SPBC3B9.02c

A:Experimental source: strain 972h-; cosmid c3B9

C:Genetics:

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 04-Mar-2000
C:Accession: T39487
R:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Lucas, M.; Gaillardin, C.
submitted to the EMBL Data Library, August 1997
A:Reference number: Z21858
A:Accession: T39487
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-263 <LVN>
A:Cross-references: EMBL:AL031349; PIDN:CAA20486.2; GSPDB:GN00067; SPDB:SPBC15D4.11c
A:Experimental source: strain 972h; cosmid c15D4
C:Genetics:
A:Gene: SPDB:SPBC15D4.11c
A:Map position: 2
A:Introns: 96/2; 147/3
C:Superfamily: Schizosaccharomyces pombe hypothetical protein SPBC15D4.11c

Query Match 10.1%; Score 82; DB 2; Length 263;
Best Local Similarity 21.7%; Pred. No. 2.6;
Matches 35; Conservative 33; Mismatches 65; Indels 28; Gaps 5;

QY 4 KLESKLVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRIFIISMVKDSQPRGMVMT 63

DB 47 KLDSELGVYKQVLDLPKKGYEKALHSFIHED-----PSLVNISALKETAKERIRVT 100

QY 64 ISVKCEKISLSCENKIISFKEMNPPDNIKDKSDIIFQORSVPGH----- 109

DB 101 VPIYSRSKSYV--QYKPIHSAEN--ENGNETSDELVFQHSIPAKVQLTNHGTILCAL 156

QY 110 ---DNKMQPESSEYEGYFLACEKERDLFKLILKKEDELGDR 147

DB 157 ILCKGMLHFDISIFSQSPNSQAFSSDL-RLILQKSKQYTR 196

RESULT 7

A:1261

probable periplasmic protein Cj1643 [imported] - Campylobacter jejuni (strain NCTC 11168)
C:Species: Campylobacter jejuni

C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 31-Mar-2000

C:Accession: A81261

R:Parkhill, J.; Wren, B.W.; Mungall, K.; Kettle, J.M.; Churcher, C.; Basham, D.; Chilling
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barre
Nature 403, 665-668, 2000

A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp
A:Reference number: A81250; MUID:20150912

A:Accession: A81261

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-364 <PAR>

A:Cross-references: GB:AL139079; GB:AL111168; NID:q6968971; PIDN:CAB73631.1; PID:q696906

A:Experimental source: serotype O2, strain NCTC 11168

C:Genetics:
A:Gene: Cj1643

Query Match 10.1%; Score 82; DB 2; Length 364;

Best Local Similarity 25.5%; Pred. No. 3.8;

Matches 39; Conservative 21; Mismatches 39; Indels 54; Gaps 9;

QY 12 IRLNDQVLFIDQGNRPLFEDMTSDCRD-NAPRIFIISMVK-----DSQPR----- 58

DB 211 LRKLEKILFADRGSTLYFQVLRDN--MDLNISTEVFAKDLKSLFNPDSKPKKITNFTS 268

QY 59 --GMAVTISVKCEKI-----SILSENKII-SFKEMNPPDNI----- 92

DB 269 NLGLTVNASLVVTKIDPKSKVSNAGFMVGDKILRVNNIILNFKEL---QNILSAGNDFS 325

QY 93 ----KDKSDIIFQORSVPGH-----DNKMQF 115

DB 326 ILIERKSTKLPLSNFENNEJGGNAGSGDGKQF 358

RESULT 8

T00679

hypothetical protein At2g43990 [imported] - Arabidopsis thaliana

N:Alternate names: hypothetical protein F6E13.12

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 23-Mar-2001

C:Accession: T00679; A84873

R:Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Syke

submitted to the EMBL Data Library, June 1998

A:Description: Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence.

A:Reference number: Z14180

A:Accession: T00679

A:Status: translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-632 <ROU>

A:Cross-references: EMBL:AC004005; NID:g3212846; PID:g3212856

A:Experimental source: cultivar Columbia

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,

cuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Water

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana

A:Reference number: A84420; MUID:20083487

A:Accession: A84873

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-632 <STO>

A:Cross-references: GB:AE002093; NID:g3212856; PIDN:AAC23407.1; GSPDB:GN00139

C:Genetics:
A:Gene: At2g43990; F6E13.12

A:Map position: 2

Query Match 9.7%; Score 79; DB 2; Length 632;

Best Local Similarity 25.6%; Pred. No. 14;

Matches 34; Conservative 30; Mismatches 39; Indels 30; Gaps 9;

QY 28 PLFEDMTSD-CDRNAPRIFIISMVKDSQPRGMVMTISVKCEK-----ISILSCENK 79

DB 368 PLSDRSASSDLNCSGRSLSPMDIYKETRR---ISSLSNPELFRFRFTHLSSCDGE 424

QY 80 IISFK-----EMNPPDNIKDKSDIIFQORSVP--GHDNKMVF--ESSSYEGYF-LACEK 129

DB 425 ASAFDTSPTCELDPSHLKDGKSSPL----SVDTLGSENVVIQTPESNSSFDNVFGLSCSQ 480

QY 130 ERDLFKLILKKED 142

DB 481 AE-----IQKKHD 488

RESULT 9

S15661

(2'-5')oligo(A) synthetase (EC 2.7.7.-) L1 - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 31-Dec-1993 #sequence_revision 02-Jun-1994 #text_change 16-Jul-1999

C:Accession: S15661; S19108

R:Rutherford, M.N.; Kumar, A.; Nissim, A.; Chebath, J.; Williams, B.R.G.

Nucleic Acids Res. 19, 1917-1924, 1991

A:Title: The murine 2-5A synthetase locus: three distinct transcripts from two linked

A:Reference number: S15660; MUID:91232962

A:Accession: S15661

A:Molecule type: mRNA

A:Residues: 1-192 <RUT>

A:Cross-references: EMBL:X55982

R:Williams, B.

A:Reference number: S19108

A:Accession: S19108

A:Molecule type: mRNA

A:Residues: 1-175, 'L', 177-192 <WIL>

A:Cross-references: EMBL:X55982; NID:g49714; PIDN:CAA39455.1; PID:g49715

C:Superfamily: oligo(A) synthetase

C:Keywords: nucleotidyltransferase

RESULT 13
T44357
hypothetical protein [Imported] - Clostridium histolyticum
C:Species: Clostridium histolyticum
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C:Accession: T44357
R:Ratsushita, O.; Jung, C.M.; Katayama, S.; Minami, J.; Takahashi, Y.; Okabe, A.
J. Bacteriol. 181, 923-933, 1999
A:Title: Gene duplication and multiplicity of collagenases in Clostridium histolyticum.
A:Reference number: 222752; MUID:99121032
A:Accession: T44357
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-204 <NAT>
A:Cross-references: EMBL:AB014075; NID:g3868863; PIDN:BAA3454.1; PID:g3892648
A:Experimental source: strain JCM 1403

Query Match 9.4%; Score 76.5; DB 2; Length 204;
Best Local Similarity 26.4%; Pred. No. 6.3;
Matches 32; Conservative 19; Mismatches 51; Gaps 5;

QY 9 LSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPTIFII--SMYKDSQPRGMAVTISV 66

25 ISTEENBNHKASSNKOCEAYTCYN---TANSCGTIVVFCVVI KDCFCNKTETVIDE 90

QV 67 KCEK-----ISILSCENKIIISFKEMNPDPNIKOTKSDIIFORSVPBGHDNKMOFESS 119

[illegible]

Qy 120 y 120

135 y 135

RESULT 14
H64245
hypothetical protein MG414 - Mycoplasma genitalium
C:Species: Mycoplasma genitalium
C:Date: 10-Nov-1995 #sequence
C:Accession: H64245; G64245
R:Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;
M.: Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.
, C.A.; Venter, J.C.
Science 270, 397-403, 1995
A:title: The minimal gene
A:Reference number: A64200; MUID:96026346
complement of Mycoplasma genitalium.

Query Match 9.4%; Score 76.5; DB 2; Length 1036;
Best Local Similarity 21.9%; Pred. NO. 43;
Matches 33; Conservative 33; Mismatches 64; Indels 21; Gaps 6;

14 NLNDQVLFIDQGNRPLFED--MTDSDCRDNAPRTIFIISMYKDSQPRGMAVTISVKCEKI 71 Qy

Db 845 SLNDEQLVVDKLNLTISEKRLQTKNVRFNLNKFNILHVENKNOFNLVDVDVRSKKL 904

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OM protein - protein search, using sw model

Run on: October 8, 2002, 10:13:54 ; Search time 15.78 Seconds
(without alignments)
385.233 Million cell updates/sec

Title: SEQ6ILEAT73

Perfect score: 815

Sequence: 1 YFGKLESKSLVIRNLDQVL.....LKKEDLGDRSIMFTVQNE 157

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	810	99.4	193	1	IL18_HUMAN
2	658	80.7	193	1	IL18_HORSE
3	653	80.1	193	1	IL18_BOVIN
4	636	78.0	192	1	IL18_PIG
5	612	75.1	193	1	IL18_CANEA
6	514	63.1	192	1	IL18_MOUSE
7	513.5	63.0	194	1	IL18_RAT
8	83.5	10.2	270	1	IL1A_PIG
9	83	10.2	267	1	IL1A_RABIT
10	78.5	9.6	192	1	OSAB_MOUSE
11	77.5	9.5	270	1	IL1A_HORSE
12	77.5	9.5	1228	1	ECM_HUMAN
13	76.5	9.4	527	1	RAG2_HUMAN
14	76.5	9.4	1036	1	Y414_MYCGE
15	75	9.2	2663	1	CENE_HUMAN
16	74.5	9.1	1663	1	CO3_MOUSE
17	74	9.1	270	1	IL1A_FELCA
18	74	9.1	426	1	YXCC_ASTLO
19	73.5	9.0	375	1	YIC5_CAEEL
20	73	9.0	467	1	M3K8_RAT
21	73	9.0	1772	1	MSPI_PLAYO
22	72.5	8.9	527	1	RAG2_RABIT
23	72	8.8	467	1	M3K8_MOUSE
24	71.5	8.8	691	1	Y104_YEAST
25	70.5	8.7	313	1	COL4_ARATH
26	70.5	8.7	644	1	YGM4_YEAST
27	70.5	8.7	711	1	TRFL_HUMAN
28	70.5	8.7	853	1	PHS1_DICDI
29	70.5	8.7	1114	1	RH18_YEAST
30	70	8.6	253	1	ADLY_ECOLI
31	70	8.6	700	1	NONA_DROME
32	70	8.6	1481	1	CFTR_BOVIN
33	70	8.6	2273	1	ABCR_HUMAN

34	70	8.6	3317	1	CADN_RAT	P58365	rattus norv
35	70	8.6	3354	1	CADN_MOUSE	Q99of4	mus musculus
36	70	8.6	4590	1	FATH_HUMAN	Q14517	homo sapien
37	69.5	8.5	268	1	IL1A_BOVIN	P08831	bos taurus
38	69.5	8.5	467	1	M3K8_HUMAN	P41279	homo sapien
39	69.5	8.5	875	1	POP1_YEAST	P41812	saccharomyc
40	69.5	8.5	1830	1	BP28_ARATH	Q9c8z4	arabidopsi
41	69	8.5	269	1	MBKE_KLEPN	P21649	klebsiella
42	69	8.5	578	1	TRML_DROME	Q9vK89	drosophila
43	69	8.5	586	1	SYD_BORBU	O51402	borrelia bu
44	68.5	8.4	268	1	IL1A_CAPHI	P79161	capra hircu
45	68.5	8.4	270	1	IL1A_MOUSE	P01582	mus musculus

ALIGNMENTS

RESULT	1	IL18_HUMAN	STANDARD;	PRT;	193 AA.
AC	Q14116;	O75599;			
DT	15-JUL-1998	{Rel. 36, Created}			
DT	15-JUL-1998	{Rel. 36, Last sequence update}			
DT	01-MAR-2002	{Rel. 41, Last annotation update}			
DE	Interleukin-18 precursor (IL-18) (Interferon-gamma inducing factor)				
DE	(IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).				
GN	IL18 OR IGIF.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Liver;				
RX	MEDLINE=96247646; PubMed=8666798;				
RA	Ushio S., Namba M., Okura T., Hattori K., Nukada Y., Akita K.,				
RA	Tanabe F., Konishi K., Micallef M., Fujii M., Torigoe K., Tanimoto T.,				
RA	Fukuda S., Ikeda M., Okamura H., Kurimoto M.;				
RT	"Cloning of the cDNA for human IFN-gamma-inducing factor, expression				
RT	in Escherichia coli, and studies on the biologic activities of the				
RT	protein.";				
RT	J. Immunol. 156:4274-4279(1996).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RA	Yong D., Guixin D., Lihua H., Haitao W.;				
RT	"Cloning and sequencing of the cDNA for precursor hIL-18.";				
RL	Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RA	Liu J., Peng X., Yuan J., Qiang B.;				
RT	"Cloning of human interleukin 18 cDNA.";				
RL	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.				
RN	[4]				
RP	SEQUENCE OF 2-193 FROM N.A.				
RC	TISSUE=Periphereal blood;				
RA	Conti B., Kim S.J., Tinti C., Chun H.S., Joh T.H.;				
RT	Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.				
CC	-!- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS				
CC	AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I				
CC	CELLS.				
CC	-!- SUBCELLULAR LOCATION: Secreted.				
CC	-!- SIMILARITY: BELONGS TO THE IL-18 FAMILY.				
CC	-----				
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CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/				
CC	or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL; D49950; BAA08706.1; -.				
DR	EMBL; AF077611; AAC27787.1; -.				

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DR EMBL; AY044641; AAK95950.1; -.
DR EMBL; U90434; AAB50010.1; -.
DR MIM; 600953; -.
DR InterPro; IPR000975; Interleukin_1.
DR SMART; SM00125; IL1; 1.
KW Cytokine.
FT PROPEP 1 36 BY SIMILARITY.
FT CHAIN 37 193 INTERLEUKIN-18.
FT CONFLICT 66 66 F -> L (IN REF. 2).
FT CONFLICT 86 86 S -> R (IN REF. 2).
FT CONFLICT 191 191 N -> S (IN REF. 2).
SQ SEQUENCE 193 AA; 22326 MW; 323C62C203788D55 CRC64;

Query Match 99.4%; Score 810; DB 1; Length 193;
Best Local Similarity 99.4%; Pred. No. 3 6e-68;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSCDRNAPRTIFIIISMYKDSQPRGM 60
DB 37 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSCDRNAPRTIFIIISMYKDSQPRGM 96

QY 61 AVTISVKCEKISILSCENKIISFKEMNPPDNKDKSDIIFFQFORSVPCHDNKMQFESSY 120
DB 97 AVTISVKCEKISILSCENKIISFKEMNPPDNKDKSDIIFFQFORSVPCHDNKMQFESSY 156

QY 121 EGYFLACEKERDLFKLLKKEDELGDGRSIMFTVQNE 157
DB 157 EGYFLACEKERDLFKLLKKEDELGDGRSIMFTVQNE 193

Query Match 99.4%; Score 810; DB 1; Length 193;
Best Local Similarity 99.4%; Pred. No. 3 6e-68;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSCDRNAPRTIFIIISMYKDSQPRGM 60
DB 37 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSCDRNAPRTIFIIISMYKDSQPRGM 96

QY 61 AVTISVKCEKISILSCENKIISFKEMNPPDNKDKSDIIFFQFORSVPCHDNKMQFESSY 120
DB 97 AVTISVKCEKISILSCENKIISFKEMNPPDNKDKSDIIFFQFORSVPCHDNKMQFESSY 156

QY 121 EGYFLACEKERDLFKLLKKEDELGDGRSIMFTVQNE 157
DB 157 EGYFLACEKERDLFKLLKKEDELGDGRSIMFTVQNE 193

RESULT 2
IL18_HORSE STANDARD; PRT; 193 AA.
AC QXASQ7;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE Interleukin-18 precursor (IL-18) (Interferon-gamma inducing factor)
DE (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).
DE IL18 OR IGIF.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
ON NCBI_TaxID=9796;
RP SEQUENCE FROM N.A.
RA Nicolson L., Penha-Goncalves M.N., Keanie J.L., Logan N.A.,
RA Argyle D.J., Onions D.E.;
RT "Nucleotide sequence of equine Interleukin 12 and 18 cDNAs.";
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CC CELLS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE IL-18 FAMILY.
CC -----
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CC -----
CC EMBL; Y11131; CAA72013.1; -.
CC KW Cytokine.
CC FT PROPEP 1 36 BY SIMILARITY.
CC FT CHAIN 37 193 INTERLEUKIN-18.
CC SQ SEQUENCE 193 AA; 22058 MW; 4D81535E9004ECAF CRC64;

Query Match 80.7%; Score 658; DB 1; Length 193;
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Best Local Similarity 77.7%; Pred. No. 4 2e-54;
Matches 122; Conservative 21; Mismatches 14; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSCDRNAPRTIFIIISMYKDSQPRGM 60
DB 37 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSCDRNAPRTIFIIISMYKDSQPRGM 96

QY 61 AVTISVKCEKISILSCENKIISFKEMNPPDNKDKSDIIFFQFORSVPCHDNKMQFESSY 120
DB 97 AVTISVKCEKISILSCENKIISFKEMNPPDNKDKSDIIFFQFORSVPCHDNKMQFESSY 156

QY 121 EGYFLACEKERDLFKLLKKEDELGDGRSIMFTVQNE 157
DB 157 EGYFLACEKERDLFKLLKKEDELGDGRSIMFTVQNE 193

RESULT 3
IL18_BOVIN STANDARD; PRT; 193 AA.
AC Q9TU73;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-18 precursor (IL-18) (Interferon-gamma inducing factor)
DE (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).
DE IL18.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
ON NCBI_TaxID=9913;
RP SEQUENCE FROM N.A.
RA MEDLINE=20012648; PubMed=10547157;
RA Shoda L.K., Zarlega D.S., Hirano A., Brown W.C.;
RT "Cloning of a cDNA encoding bovine interleukin-18 and analysis of IL-
RT 18 expression in macrophages and its IFN-gamma-inducing activity.";
RL J. Interferon Cytokine Res. 19:1169-1177(1999).
CC -1- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CC CELLS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE IL-18 FAMILY.
CC -----
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CC -----
CC EMBL; AF124789; AAF08686.1; -.
CC DR InterPro; IPR000975; Interleukin_1.
CC DR SMART; SM00125; IL1; 1.
CC KW Cytokine.
CC FT PROPEP 1 36 BY SIMILARITY.
CC FT CHAIN 37 193 INTERLEUKIN-18.
CC SQ SEQUENCE 193 AA; 22347 MW; 65720F199DEA49C4 CRC64;

Query Match 80.1%; Score 653; DB 1; Length 193;
Best Local Similarity 77.1%; Pred. No. 1 2e-53;
Matches 121; Conservative 23; Mismatches 13; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSCDRNAPRTIFIIISMYKDSQPRGM 60
DB 37 HFGKLEPKLSIIRNLNDQVLFIDQGNRPLFEDMTDSCDRNAPRTIFIIISMYKDSQPRGM 96

QY 61 AVTISVKCEKISILSCENKIISFKEMNPPDNKDKSDIIFFQFORSVPCHDNKMQFESSY 120
DB 97 AVTISVKCKMSTLSCENKIVSFKEMNPPDNIDNEESDIIFFQFORSVPCHDNKMQFESSY 156
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=96061009; PubMed=7477296;
RA Okamura H., Tsutui H., Komatsu T., Yutsudo M., Hakura A.,
RA Tanimoto T., Torigoe K., Okura T., Nakada Y., Hattori K.,
RA Akita K., Namba M., Tanabe F., Konishi K., Fukuda S., Kurimoto M.;
RT "Cloning of a new cytokine that induces IFN-gamma production by T
RT cells.";
RL Nature 378:88-91(1995).
RN [2]
RC SEQUENCE OF 1-191 FROM N.A.
RC STRAIN=MOD; TISSUE=Pancrreas;
RX MEDLINE=9717346; PubMed=9022080;
RA Rothe H., Jenkins N.A., Copeland N.G., Kolb H.;
RT "Active stage of autoimmune diabetes is associated with the
RT expression of a novel cytokine, IGIF, which is located near Idd2.";
RL J. Clin. Invest. 99:469-474(1997).
CC -!- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CC CELLS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE IL-18 FAMILY.
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CC -----
DR EMBL; D49949; BAA08705.1; -.
DR EMBL; U66244; AAB49753.1; -.
DR MGD; MGI:107936; IL18.
DR InterPro: IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR SMART; SM00125; IL1; 1.
KW Cytokine.
FT PROPEP 1 35
FT CHAIN 36 192 INTERLEUKIN-18.
FT CONFLICT 183 185 MFT -> IS (IN REF. 2).
FT SEQUENCE 192 AA; 22135 MW; 8FED938473874D63 CRC64;
SQ
Query Match 63.1%; Score 514; DB 1; Length 192;
Best Local Similarity 64.9%; Pred. No. 8.9e-41;
Matches 100; Conservative 27; Mismatches 25; Indels 2; Gaps 2;
QY 2 FGKLESKLVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIIISMYKDSQPRGMA 61
DB 37 FGRLHCTTAVIRNLNDQVLFVDK-RQVFEDMTDIDQSAPEQTRLIYYMYKDSVIRGLA 95
QY 62 VTSVKCEKISLSCENKISFKEMNPPDNKDKSIIFQFORSVPGHDKMKOFESSYE 121
DB 96 VTLVSKDSKSTLSCKNKIISFEMDPENIDDIQSDLIFFQKRVPGH-NKMEFEESLYE 154
QY 122 GYFLACERDLFKILKKEDELGDRSIMFTVQN 155
DB 155 GHFLACQKEDDAFKLILKKKDKNGDKSVMTLTN 188
RESULT 7
IL18_RAT
ID IL18_RAT STANDARD; PRT; 194 AA.
AC P97636; p97637; O88749;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-18 precursor (IL-18) (interferon-gamma inducing factor)

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DE (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).
GN IL18 OR IGIF.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Adrenal gland;
RX MEDLINE=97152963; PubMed=8999896;
RA Conti B., Jahng J.W., Tinti C., Son J.H., Joh T.H.;
RT "Induction of interferon-gamma inducing factor in the adrenal
RT cortex.";
RL J. Biol. Chem. 272:2035-2037(1997).
RN [2]
RC SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain;
RX MEDLINE=98368130; PubMed=9702748;
RA Culhane A.C., Hall M.D., Rothwell N.J., Luheshi G.N.;
RT "Cloning of rat brain interleukin-18 cDNA.";
RL Mol. Psych. 3:362-366(1998).
CC -!- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CC CELLS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE IL-18 FAMILY.
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CC -----
DR EMBL; U77776; AAC53009.1; -.
DR EMBL; U77777; AAC53010.1; -.
DR EMBL; AJ222813; CAAL1001.1; -.
DR InterPro: IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR SMART; SM00125; IL1; 1.
KW Cytokine; Alternative splicing.
FT PROPEP 1 36 BY SIMILARITY.
FT CHAIN 37 194 INTERLEUKIN-18.
FT VARSPLIC 121 139 MISSING (IN ISOFORM ALPHA).
FT CONFLICT 4 5 MS -> IP (IN REF. 2).
FT CONFLICT 48 48 I -> M (IN REF. 2).
FT SEQUENCE 194 AA; 22303 MW; E2089AD6F1798450 CRC64;
SQ
Query Match 63.0%; Score 513.5; DB 1; Length 194;
Best Local Similarity 63.2%; Pred. No. 1e-40;
Matches 98; Conservative 28; Mismatches 28; Indels 1; Gaps 1;
QY 1 YFKLESKLVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIIISMYKDSQPRGM 60
DB 37 HFGRHCTTAVIRNLNDQVLFVDKRNPPVPEMDPIDRTANESQTRLIYYMYKDSVIRGL 96
QY 61 AVTSVKCEKISLSCENKISFKEMNPPDNKDKSIIFQFORSVPGHDKMKOFESSY 120
DB 97 AVTLVSKDGRMSTLSCKNKIISFEMNPPENIDDIKSLIFFQKRVPGH-NKMEFEESLY 155
QY 121 EGYFLACERDLFKILKKEDELGDRSIMFTVQN 155
DB 156 EGFLACQKEDDAFKLVLRKDKNGDKSVMTLTN 190
RESULT 8
IL1A_PIG
ID IL1A_PIG STANDARD; PRT; 270 AA.
AC P18430;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)

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KW Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
FT PROPEP 1 112 BY SIMILARITY.
FT CHAIN 113 270 INTERLEUKIN-1 ALPHA.
FT CARBOHYD 141 141 N-LINKED (GLCNAC...) (POTENTIAL).
FT CONFLICT 110 110 R -> K (IN REF. 2).
FT CONFLICT 150 150 G -> V (IN REF. 2).
SQ SEQUENCE 270 AA; 30806 MW; 381859713754DB90 CRC64;

Query Match
Best Local Similarity 9.5%; Score 77.5; DB 1; Length 270;
Matches 28; Conservative 31; Mismatches 60; Indels 11; Gaps 4;

QY 7 SKLSVIRNLNDQVLFDGIDGNRPLFEDMTDSCDRNAPRTI-----FIISMVKDSDPRGMA 61
DB 122 TKNYEMRIVNHQCTLNDALNGSVIRDTSGQYLATLALNLDLDAVDFMGATSEDSQLP 181
QY 62 VTISVKCEKISI-LSCENKIISFKEM-NPPDNIKPTKSDIIFQSVFGHONKMFESS 119
DB 182 VTLRISKTRLFVSAQNEDEPVLKKEMPTPKTIKDTNLLFFWER----HGSKNYFKSVA 237
QY 120 YEGYELACEK 129
DB 238 HPKLFIAATKQ 247

RESULT 12
ECM_HUMAN STANDARD; PRT; 1228 AA.
AC Q13201;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Endothelial cell multimerin precursor.
GN MMRN OR ECM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 368-376.
RC TISSUE=Endothelial cells;
RA Hayward C.P.M., Hassell J.A., Denomme G.A., Rachubinski R.A.,
RA Brown C., Kelton J.G.;
RT "The cDNA sequence of human endothelial cell multimerin. A unique
RT protein with RGDS, coiled-coil, and epidermal growth factor-like
RT domains and a carboxyl terminus similar to the globular domain of
RT complement C1q and collagen type VIII and X."
RL J. Biol. Chem. 270:18246-18251(1995).
CC -1- FUNCTION: CARRIER PROTEIN FOR PLATELET (BUT NOT PLASMA) FACTOR
CC V/Va. MAY PLAY A ROLE IN THE STORAGE AND STABILIZATION OF FACTOR V
CC IN PLATELETS.
CC -1- SUBUNIT: MULTIMERIC. COMPOSED OF VARYING SIZED, DISULFIDE-LINKED
CC MULTIMERS, THE SMALLEST OF WHICH IS A HOMOTRIMER. PROTEOLYSIS OF
CC THE PROMULTIMERIN IN THE N-TERMINAL REGION, LEADS TO THE MATURE
CC P155 FORM THAT IS STORED IN PLATELETS.
CC -1- TISSUE SPECIFICITY: SYNTHESIZED BY ENDOTHELIAL CELLS AND
CC MEGAKARYOCYTES. STORED IN PLATELET ALPHA GRANULES AND ENDOTHELIAL
CC CELL WEIBEL-PALADE BODIES, FOLLOWING ACTIVATION OF THESE CELLS, IT
CC IS RELEASED AND ATTACHED TO MEGAKARYOCYTES, PLATELETS, ENDOTHELIUM
CC AND SUBENDOTHELIUM OF BLOOD VESSELS. NOT FOUND IN PLASMA. FOUND IN
CC VASCULAR TISSUES SUCH AS PLACENTA, LUNG, AND LIVER.
CC -1- PTM: THE N-TERMINUS IS BLOCKED.
CC -1- PTM: EXTENSIVELY N-GLYCOSYLATED.
CC -1- DISEASE: DEFICIENCY IN MULTIMERIN DUE TO PROTEOLYTIC DEGRADATION
CC WITHIN THE PLATELET ALPHA GRANULES IS ASSOCIATED WITH AN AUTOSOMAL
CC DOMINANT BLEEDING DISORDER (FACTOR V QUEBEC).
CC -1- SIMILARITY: CONTAINS 1 C1Q DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
CC -----
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EMBL; U27109; AAC52065.1; -.
DR MIN; 601456; -.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001073; C1q.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF_2.
DR Pfam; PF00008; EGF; 1.
DR PRINTS; PR00007; COMPLEMNTC1Q.
DR SMART; SM00110; C1Q; 1.
DR SMART; SM00181; EGF; 1.
DR PROSITE; PS01113; C1Q; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
KW Signal; Glycoprotein; EGF-like domain; Coiled coil.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 1228 ENDOTHELIAL CELL MULTIMERIN.
FT DOMAIN 1041 1077 EGF-LIKE.
FT DOMAIN 1119 1149 C1Q.
FT DOMAIN 333 365 COILED COIL (POTENTIAL).
FT DOMAIN 400 430 COILED COIL (POTENTIAL).
FT DOMAIN 503 523 COILED COIL (POTENTIAL).
FT DOMAIN 580 650 COILED COIL (POTENTIAL).
FT DOMAIN 675 726 COILED COIL (POTENTIAL).
FT DOMAIN 819 869 COILED COIL (POTENTIAL).
FT DOMAIN 309 313 POLY-SR.
FT SITE 186 188 CELL ATTACHMENT SITE (POTENTIAL).
FT DISULFID 1045 1056 BY SIMILARITY.
FT DISULFID 1050 1065 BY SIMILARITY.
FT CARBOHYD 21 21 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 97 97 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 114 114 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 120 120 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 344 344 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 431 431 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 507 507 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 541 541 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 576 576 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 618 618 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 680 680 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 729 729 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 783 783 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 816 816 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 828 828 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 840 840 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 921 921 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 933 933 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 942 942 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 981 981 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 1020 1020 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 1075 1075 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 1228 AA; 138071 MW; EAA98B0A17E2C4CD CRC64;

Query Match
Best Local Similarity 9.5%; Score 77.5; DB 1; Length 1228;
Matches 32; Conservative 37; Mismatches 46; Indels 35; Gaps 9;

QY 1 YFGKLESKLSVIRNLNDQVL-----FIDQGNRPLFEDMTD-----SDCRDNAPR-TIFII 49
DB 502 YVESLNKTLKSLKEVHEQLLSTEQVSDQKNAPAAESVNNVTEYWTSLHENIKKQSLMWL 561
QY 50 SMYKD---SQPRGMVAVTSVCKEKISII-SCENKI-----ISFKEMPPDN---IKDTK 96
DB 562 OMFEDLHQESKINNLTVSLMEKESLRGECEDMLSKCRNDFKQFKDTEENLHVLNQTLL 621
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QY 97 SDIIFORSVPGHDKM-----QFESSYE 121
DB 622 AEVLFF-----PMDNKKMKMSEQLNDLTYD 645

RESULT 13
RAG2_HUMAN STANDARD; PRT; 527 AA.
ID RAG2_HUMAN STANDARD; PRT; 527 AA.
AC P5895;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE V(D)J recombination activating protein 2 (RAG-2).
GN RAG2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=93052553; PubMed=1428003;
RA Ichihara Y., Hirai M., Kurosawa Y.;
RT "Sequence and chromosome assignment to llp13-p12 of human RAG genes.";
RL Immunol. Lett. 33:277-284(1992).
RN [2]
RP SEQUENCE OF 318-411 FROM N.A.
RX MEDLINE=92003959; PubMed=1832998;
RA Borjes J.C., Cayuela J.M., Loiseau P., Sigaux F.;
RT "Expression of human recombination activating genes (RAG1 and RAG2)
RT in neoplastic lymphoid cells: correlation with cell differentiation
RT and antigen receptor expression.";
RL Blood 78:2053-2061(1991).
RN [3]
RP VARIANTS SCID GLN-229 AND TYR-478.
RX MEDLINE=96412253; PubMed=8810255;
RA Schwarz K., Gauss G.H., Ludwig L., Pannicke U., Li Z., Linder D.,
RA Friedrich W., Seger R.A., Hansen-Hagge T.E., Desiderio S.,
RA Lieber M.R., Bartram C.R.;
RT "RAG mutations in human B cell-negative SCID.";
RL Science 274:97-99(1996).
RN [4]
RP VARIANTS OS TRP-41 AND ARG-285.
RX MEDLINE=98292185; PubMed=9630231;
RA Villa A., Santagata S., Bozzi F., Gilliani S., Frattini A., Imberti L.,
RA Gatta L.B., Ochs H.D., Schwarz K., Notarangelo L.D., Vezzoni P.,
RA Spanopoulou E.;
RT "Partial V(D)J recombination activity leads to Omenn syndrome.";
RL Cell 93:885-896(1998).
CC -1- FUNCTION: DURING LYMPHOCYTE DEVELOPMENT, THE GENES ENCODING
CC IMMUNOGLOBULINS AND T CELL RECEPTORS ARE ASSEMBLED FROM VARIABLE
CC (V), DIVERSITY (D), AND JOINING (J) GENE SEGMENTS. THIS
CC COMBINATORIAL PROCESS, KNOWN AS V(D)J RECOMBINATION, ALLOWS THE
CC GENERATION OF AN ENORMOUS RANGE OF BINDING SPECIFICITIES FROM A
CC LIMITED AMOUNT OF GENETIC INFORMATION. THE RAG1/RAG2 COMPLEX
CC INITIATES THIS PROCESS BY BINDING TO THE CONSERVED RECOMBINATION
CC SIGNAL SEQUENCES (RSS) AND INTRODUCING A DOUBLE-STRAND BREAK
CC BETWEEN THE RSS AND THE ADJACENT CODING SEGMENT. THESE BREAKS ARE
CC GENERATED IN TWO STEPS, NICKING OF ONE STRAND (HYDROLYSIS),
CC FOLLOWED BY HAIRPIN FORMATION (TRANSESTERIFICATION). RAG1/2 HAS
CC ALSO BEEN SHOWN TO FUNCTION AS A TRANSPOSASE IN VITRO, AND TO
CC POSSESS RSS-INDEPENDENT ENDONUCLEASE ACTIVITY (END PROCESSING) AND
CC HAIRPIN OPENING. RAG1 ALONE CAN BIND TO RSS BUT STABLE, EFFICIENT
CC BINDING REQUIRES RAG2. ALL KNOWN CATALYTIC ACTIVITIES REQUIRE THE
CC PRESENCE OF BOTH PROTEINS.
CC -1- SUBUNIT: THE RAG COMPLEXES APPEAR TO CONTAIN THREE TO FIVE
CC MOLECULES OF RAG2 FOR EACH MOLECULE OF RAG1.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- TISSUE SPECIFICITY: CELLS OF THE B AND T LYMPHOCYTE LINEAGES.
CC -1- DISEASE: DEFECTS IN RAG2 ARE A CAUSE OF SEVERE COMBINED
CC IMMUNODEFICIENCY, B CELL-NEGATIVE (B(-) SCID).
CC -1- DISEASE: DEFECTS IN RAG2 ARE A CAUSE OF OMENN SYNDROME (OS); A

SEVERE IMMUNODEFICIENCY CHARACTERIZED BY THE PRESENCE OF
ACTIVATED, ANERGIC, OLIGOCLONAL T CELLS, HYPEROSINOPHILIA, AND
HIGH IGE LEVELS.
-1- DATABASE: NAME=RAG2base; NOTE=RAG2 deficiency database;
WWW="http://www.uta.fi/imt/bioinfo/RAG2base/"
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CC EMBL; M94633; ; NOT_ANNOTATED_CDS.
CC MIM; 179616;
CC MIM; 601457;
CC MIM; 603554;
CC InterPro; IPR004321; RAG2.
CC Pfam; PF03089; RAG2; 1.
CC Hydrolase; Endonuclease; Nuclear protein; DNA-binding;
CC DNA recombination; Disease mutation.
CC VARIANT 41 41 C->W (IN OS).
CC VARIANT 229 229 /FTID-VAR_008895.
CC FTID-VAR_008895.
CC VARIANT 285 285 /FTID-VAR_005570.
CC FTID-VAR_005570.
CC VARIANT 478 478 /FTID-VAR_008896.
CC FTID-VAR_008896.
CC FTID-VAR_005571.
CC FTID-VAR_005571.
CC SEQUENCE 527 AA; 59241 MW; ICC4D0F8635BA87 CRC64;

Query Match 9.4%; Score 76.5; DB 1; Length 527;
Best Local Similarity 28.9%; Pred. No. 9.3;
Matches 26; Conservative 10; Mismatches 31; Indels 23; Gaps 4;

QY 72 SILSCENKISFKEMPNPNKIKTSDIIFQRS-----VPGHDKMKQFESSYEG 122
DB 288 NIISLEDNKIEIREMETPTDTPDKIKSKIWFSGSNMGNTVFLGIPG-DNK-QVVSCEGYF 345
QY 123 YFLACEKERDLFLKILKKEDELGRSINF 152
DB 346 YMLKC-----AEDDTNEEQTTFT 363

RESULT 14
Y414_MYCGE STANDARD; PRT; 1036 AA.
AC P47653; P47654; Q49457;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MG414.
GN MG414.
OS Mycoplasma genitalium.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
OC Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33530 / G-37;
RX MEDLINE=96026346; PubMed=7569993;
RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
RA Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
RA Fritchmann J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,
RA Nguyen D.T., Ufferback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
RA Tomb J.-F., Dougherty B.A., Bost K.F., Hu P.-C., Lucier T.S.,
RA Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
RT "The minimal gene complement of Mycoplasma genitalium.";
RL Science 270:397-403(1995).
RN [2]
RP SEQUENCE OF 52-146 AND 733-833 FROM N.A.

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```
RC STRAIN=ATCC 33530 / G-37;
RA MEDLINE=94075230; PubMed=8253680;
RX Peterson S.N., Hu P.-C., Bott K.F., Hutchison C.A. III;
RT "A survey of the Mycoplasma genitalium genome by using random
RL sequencing.";
RJ J. Bacteriol. 175:7918-7930(1993).
CC -|- SIMILARITY: BELONGS TO THE MG414 / MG415 FAMILY.
CC -----
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CC -----
DR EMBL; U39723; AAC71641.1; -.
DR EMBL; U01695; AAB01008.1; -.
DR EMBL; U01804; AAD12330.1; -.
DR TIGR; MG414; -.
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 4 24
FT TRANSMEM 1004 1024
FT CONFLICT 733 736
FT CONFLICT LEPT -> SRAS (IN REF. 2).
SQ SEQUENCE 1036 AA; 123179 MW; 12A21F00F686A141 CRC64;

Query Match          9.4%; Score 76.5; DB 1; Length 1036;
Best Local Similarity 21.9%; Pred. No. 21;
Matches 33; Conservative 33; Mismatches 64; Indels 21; Gaps 6;

QY 14 NLNDQVLFIDQGNRPLFED--MTDSDCRDNPRTIFIIISMYKDSQPRGMVATISYKCEKI 71
DB 845 SLNDEQLLVKLNITLSEKRLQTTNRFNKNKFNHVLNKNQFNLFVDVVRSKRL 904
QY 72 SI--LSCENKIISFKEMPPDNKDKSDIIFQFQSVFGHDKNQFESSSEYGYFLACEK 129
DB 905 FIKGVNNDNQVSIY-----DLKITNNQTLIV-DANGFDNSIWFDTIS-----EN 950
QY 130 ERDLFKLI---LKKEDELGDRSIMFTVQNEED 157
DB 951 QTQLFKAUSFYLKQNNLOFKRVPDFNLKSQD 981

RESULT 15
CENE_HUMAN
ID CENE_HUMAN STANDARD; PRT: 2663 AA.
AC Q02224;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Centromeric protein E (CENP-E protein).
GN CENPE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93024922; PubMed=1406971;
RA Yen T.J., Li G., Schaar B.T., Szilak I., Cleveland D.W.;
RT "CENP-E is a putative kinetochore motor that accumulates just before
RT mitosis.";
RL Nature 359:536-539(1992).
RN [2]
RP CHARACTERIZATION.
RX MEDLINE=95196755; PubMed=7889940;
RA Thowar D.A., Jordan M.A., Schaar B.T., Yen T.J., Wilson L.;
RT "Mitotic HeLa cells contain a CENP-E-associated minus end-directed
RT microtubule motor.";
RL EMBO J. 14:918-926(1995).
RN [3]
RP CHARACTERIZATION.

RX MEDLINE=98437347; PubMed=9763420;
RA Chan G.K.T., Schaar B.T., Yen T.J.;
RT "Characterization of the kinetochore binding domain of CENP-E reveals
RT interactions with the kinetochore proteins CENP-F and HUBB1.";
RJ J. Cell Biol. 143:49-63(1998).
CC -|- FUNCTION: MINUS-END DIRECTED MICROTUBULE MOTOR. PROBABLE
CC KINETOCORE MOTOR. ACCUMULATES JUST BEFORE MITOSIS AT THE G2 PHASE
CC OF THE CELL CYCLE. PROBABLY IMPORTANT FOR CHROMOSOME MOVEMENT
CC AND/OR SPINDLE ELONGATION.
CC -|- SUBUNIT: INTERACTS WITH CENP-F AND BUBR1 KINASE.
CC -|- SUBCELLULAR LOCATION: ASSOCIATES WITH KINETOCHORES DURING
CC CONGRESSION, RELOCATES TO THE SPINDLE MIDZONE AT ANAPHASE, AND IS
CC QUANTITATIVELY DISCARDED AT THE END OF THE CELL DIVISION.
CC -|- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY.
CC -----
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CC -----
DR EMBL; Z15005; CAA78727.1; -.
DR PIR; S28261; S28261.
DR HSSP; P17119; 3KAR.
DR MIM; 117143; -.
DR InterPro; IPR001752; kinesin.
DR Pfam; PF00225; kinesin_1.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM00129; KISC. 1.
DR PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
DR PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
KW Motor protein; Cell division; ATP-binding; Coiled coil; Mitosis;
KW Cell cycle; Centromere.
FT DOMAIN 1 335
FT DOMAIN 336 2471
FT DOMAIN 2472 2663
FT NP_BIND 86 93
FT NP_BIND ATP (BY SIMILARITY).
SQ SEQUENCE 2663 AA; 312087 MW; CFC13880C8C8CB8 CRC64;

Query Match          9.2%; Score 75; DB 1; Length 2663;
Best Local Similarity 20.6%; Pred. No. 90;
Matches 37; Conservative 38; Mismatches 69; Indels 36; Gaps 7;

QY 4 KLESKLSVIRNLNDQVLFIDQGNRPL--FEDWTDSDCRDNPRTIFIIISMYKDSQPRGMA 61
DB 916 KLQOTLEEVKTLTQEKDDLKQLQESLQTERDQLKSDIHD-----VNMNIDTQELRN 968
QY 62 VTISVKCEKISILSCENKIIS--FKEMPPDNKDKSDIIFQFQSVFGHDKNQFESS 119
DB 969 ALESKLQHQETINTLTKSISEVSRNLHMEENTGETKDE---FOQKMGVIGDKODLEAKN 1025
QY 120 YGYEFL-----ACEKRDLFKLIUKK-----EDELGDR-----SIMFTVQNEED 157
DB 1026 TOTLTADVKDNEITEEQRKIFSLIOEKNELOQMLESVTAKEQLKTDLENIENTIENQ 1085

Search completed: October 8, 2002, 10:17:03
Job time: 189 sec
```


GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 8, 2002, 10:13:29 ; Search time 43.19 Seconds
(without alignments)
628.854 Million cell updates/sec

Title: SEQ6ILEAT73
Perfect score: 815
Sequence: 1 YFGKLESKLSVIRNLNDQVL.....LKKDELGDRSIMFTVQNE 157

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTREMBL19:*
- 1: sp_archaea:*
 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
 - 6: sp_mammal:*
 - 7: sp_mhc:*
 - 8: sp_organelle:*
 - 9: sp_phase:*
 - 10: sp_plant:*
 - 11: sp_rodent:*
 - 12: sp_virus:*
 - 13: sp Vertebrate:*
 - 14: sp Unclassified:*
 - 15: sp_virus:*
 - 16: sp_bacteriap:*
 - 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	797	97.8	193	4 Q96KJ8	Q96KJ8 homo sapien
2	791	97.1	193	6 Q9BG15	Q9BG15 macaca mula
3	653	80.1	178	6 Q9M2L8	Q9M2L8 bos taurus
4	647	79.4	193	6 Q9GL09	Q9GL09 ovis aries
5	633	77.7	192	6 Q95M33	Q95M33 felis silve
6	625	76.7	192	6 Q9N1P7	Q9N1P7 sus scrofa
7	440	54.0	196	11 Q91Z66	Q91Z66 sigmodon hi
8	312	38.3	84	6 Q95LE7	Q95LE7 canis famil
9	204	25.0	45	4 Q9N049	Q9N049 homo sapien
10	193	23.7	211	13 Q98S01	Q98S01 anas platyr
11	182.5	22.4	198	13 Q91BD2	Q91BD2 gallus gall
12	91	11.2	4643	5 Q9VW71	Q9VW71 drosophila
13	84	10.3	381	3 O43031	O43031 schizosacch
14	84	10.3	452	16 O25249	O25249 helicobacte
15	83.5	10.2	866	16 O84500	O84500 chlamydia t
16	82.5	10.1	1049	2 Q93KF0	Q93KF0 caldicellul

17	82	10.1	263	3	O74316	schizosacch
18	82	10.1	364	16	Q9PM33	campylobact
19	81.5	10.0	617	5	Q25986	plasmodium
20	81	9.9	1044	5	Q94173	pneumocysti
21	80.5	9.9	454	6	Q9BGD1	micronycter
22	80	9.8	847	4	Q9NUC1	homo sapien
23	79.5	9.8	454	6	Q9BGA4	erophylla s
24	79.5	9.8	454	6	Q9BGA8	sturnira li
25	79	9.7	632	10	O80569	arabidopsis
26	78.5	9.6	454	6	Q9BGB7	phylostomu
27	78	9.6	445	13	O57610	scyllorhina
28	78	9.6	473	5	O16673	caenorhabdi
29	77.5	9.5	454	6	Q9BGB8	phyllonycte
30	76.5	9.4	137	5	O77077	plasmodium
31	76.5	9.4	204	2	Q9ZNJ7	ciostidium
32	76.5	9.4	454	6	Q9BGE3	furiperus
33	76.5	9.4	454	6	Q9BGD7	lonchorhina
34	76.5	9.4	454	6	Q9BGD5	macrotus ca
35	76.5	9.4	595	10	Q9SDM4	dunaliella
36	76	9.3	273	10	Q9LM98	arabidopsis
37	76	9.3	450	16	Q9ZLW8	helicobacte
38	76	9.3	614	10	Q9LAW0	arabidopsis
39	76	9.3	747	10	O82393	arabidopsis
40	75.5	9.3	454	6	Q9BDE1	micronycter
41	75.5	9.3	454	6	Q9BGF9	ariteus fla
42	75.5	9.3	454	6	Q9BGE7	diphylla ec
43	75.5	9.3	454	6	Q9BGD6	macrophyllu
44	75.5	9.3	454	6	Q9BGD4	macrotus wa
45	75.5	9.3	454	6	Q9BGD3	macrotus wa

ALIGNMENTS

RESULT 1

Q96KJ8 ID Q96KJ8 PRELIMINARY; PRT; 193 AA.
AC Q96KJ8;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE INTERLEUKIN 18.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ying P., Jianxin L.;
RT "Cloning of Mutant Human Interleukin 18 cDNA."
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF380360; AAK57024.1; -.
SQ SEQUENCE 193 AA; 22323 MW; 2E500205D1B7E5F7 CRC64;

Query Match	97.8%	Score 797;	DB 4;	Length 193;
Best Local Similarity	97.5%;	Pred. No. 1.7e-72;		
Matches 153;	Conservative 2;	Mismatches 2;	Indels 0;	Gaps 0;
Qy 1	YFGKLESKLSVIRNLNDQVLFTDQGNRPLFEDMTDSCDRDNAPRTFTISMYKDSQPRGM 60			
Db 37	YFGKLESKLSVIRNLNNQVLFDQGNRPLFEDMTDSCDRDNAPRTFTISMYKDSQPRGM 96			
Qy 61	AVTISVKEKISILSCENKIISFKEMNPPDNIKDKTSIIFFQRSVPGHNDKMQFESSY 120			
Db 97	AVTISVKEKISTLSCENKIISFKVNPPDNIKDKTSIIFFQRSVPGHNDKMQFESSY 156			
Qy 121	EGYFTACKEKRDFLKILKKEDELGDRSIMFTVQNE 157			
Db 157	EGYFTCEKERDFLKILKKEDELGDRSIMFTVQNE 193			
RESULT 2				

```

Q9BG15
ID Q9BG15 PRELIMINARY; PRT; 193 AA.
AC Q9BG15;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE INTERLEUKIN-18.
GN IL18.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21229850; PubMed=11331040;
RA Glavedoni L.D., Imhoof J.D., Parodi L.M., Velasquillo C.M.,
RA Hodara V.L.;
RT "Expression of the Interleukin-18 Gene from Rhesus Macaque by the
RT Simian Immunodeficiency Virus Does Not Result In Increased Viral
RT Replication.";
RL J. Interferon Cytokine Res. 21:173-180(2001).
DR EMBL; AF303732; AAK13416.1; -.
DR SEQUENCE 193 AA; 22325 MW; B2BD29C033BB0B5E CRC64;

Query Match 97.1%; Score 791; DB 6; Length 193;
Best Local Similarity 95.5%; Pred. No. 6.8e-72;
Matches 150; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSCRDNAPRTIFIISMYKDSQPRGM 60
DB 37 YFGKLESKLSIRNLNDQVLFIDQGNRPLFEDMTDSCRDNAPRTIFIINMYKDSQPRGM 96
QY 61 AVTISVKCEKISILSCENKIISFKEMNPPDNIDKTSDIIFQFORSVPGHDKNQFESSY 120
DB 97 AVAISVKCEKISTLSCENKIISFKEMNPPDNIDKTSDIIFQFORSVPGHDKNQFESSY 156
QY 121 EGYFLACEKERDLPFKLLKKEDELGDRSIMFTVQNE 157
DB 157 EGYFLACEKERDLPFKLLKKEDELGDRSIMFTVQNE 193

RESULT 3
ID Q9MZL8 PRELIMINARY; PRT; 178 AA.
AC Q9MZL8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE INTERLEUKIN-18 (FRAGMENT).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovoidea; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=KIDNEY, LIVER, BLOOD MONONUCLEAR CELLS;
RA Olsen S.C., Lee I.K., Mwangi S.M., Kehrli M., Bolin C.A.;
RT "Cloning of bovine interleukin-18, expression in Escherichia coli, and
RT characterization of the biologic activities of the recombinant
RT cytokine.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF173175; AAF89833.1; -.
DR InterPro; IPR000975; Interleukin_1.
DR SMART; SM00125; IL1; 1.
FT NON_TER 178
FT SEQUENCE 178 AA; 20631 MW; 816D6B2B88ACB497 CRC64;

Query Match 80.1%; Score 653; DB 6; Length 178;

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Best Local Similarity 77.1%; Pred. No. 4.8e-58;
Matches 121; Conservative 23; Mismatches 13; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSCRDNAPRTIFIISMYKDSQPRGM 60
DB 22 HFGKLEPKLSIRNLNDQVLFIDQGNRPLFEDMTDSCRDNAPRTIFIISMYKDSLTRGL 81
QY 61 AVTISVKCEKISILSCENKIISFKEMNPPDNIDKTSDIIFQFORSVPGHDKNQFESSY 120
DB 82 AVTISVQCKMSTLSCENKIISFKEMNPPDNIDNEESDIIFQFORSVPGHDKIQFESSLY 141
QY 121 EGYFLACEKERDLPFKLLKKEDELGDRSIMFTVQNE 157
DB 142 KGYFLACKKENDLPFKLLKQDDNDRKSVMTVQNON 178

RESULT 4
ID Q9GL09 PRELIMINARY; PRT; 193 AA.
AC Q9GL09;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE INTERLEUKIN-18 (IGIF).
GN IL-18.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovoidea; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RA Bailey S.L., Gossner A., Dalziel R., Hopkins J.;
RT "Cloning of Ovine interleukin 18 cDNA";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ401033; CAC09326.2; -.
DR InterPro; IPR000975; Interleukin_1.
DR SMART; SM00125; IL1; 1.
DR SEQUENCE 193 AA; 22166 MW; CCDOA329062EF18C CRC64;

Query Match 79.4%; Score 647; DB 6; Length 193;
Best Local Similarity 77.7%; Pred. No. 2.1e-57;
Matches 122; Conservative 20; Mismatches 15; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSCRDNAPRTIFIISMYKDSQPRGM 60
DB 37 HFGKLEPKLSIRNLNDQVLFISQGNQPVFEDMPDSCSDNAPQTIFIISMYKDSLTRGL 96
QY 61 AVTISVKCEKISILSCENKIISFKEMNPPDNIDKTSDIIFQFORSVPGHDKNQFESSY 120
DB 97 AVTISVQCKMSTLSCENKIISFKEMNPPDNIDNEESDIIFQFORSVPGHDKIQFESSLY 156
QY 121 EGYFLACEKERDLPFKLLKKEDELGDRSIMFTVQNE 157
DB 157 KGYFLACKKENDLPFKLLKQDDNDRKSVMTVQNON 193

RESULT 5
ID Q95M33 PRELIMINARY; PRT; 192 AA.
AC Q95M33;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE INTERFERON-GAMMA INDUCING FACTOR.
GN IGIF.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.

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Q9NQ49
ID Q9NQ49 PRELIMINARY; PRT; 45 AA.
AC Q9NQ49
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE INTERLEUKIN-18 (FRAGMENT).
GN IL-18.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Farhan A.J., Pravica V., Hutchinson I.V.;
RT "Identification of Human Interleukin-18 gene polymorphisms.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ295724; CAC01436.1; -
FT NON_TER 1 45
FT TER 45 45
SQ SEQUENCE 45 AA; 5266 MW; DF3A626507E3D61A CRC64;

Query Match 25.08; Score 204; DB 4; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.5e-13;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDVLFIDOGNRPFLFEDMTDSDCR 39
Db 7 YFGKLESKLSVIRNLNDVLFIDOGNRPFLFEDMTDSDCR 45

RESULT 10
Q98SQ1
ID Q98SQ1 PRELIMINARY; PRT; 211 AA.
AC Q98SQ1
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE INTERLEUKIN-18 (FRAGMENT).
GN IL-18.
OS Anas platyrhynchos (Domestic duck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
OX NCBI_TaxID=8839;
RN [1]
RP SEQUENCE FROM N.A.
RA Chan W.-S., Warr G.W., Middleton D.L., Lundquist M.L., Higgins D.A.;
RT "Anas platyrhynchos T-cell antigens, IL-18 gene.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF336122; AAK26322.1; -
DR InterPro; IPR000975; Interleukin_1.
DR SMART; SM00125; IL1; 1.
FT NON_TER 1 1
FT TER 1 1
SQ SEQUENCE 211 AA; 24541 MW; CA6FC63538211B2B CRC64;

Query Match 23.7%; Score 193; DB 13; Length 211;
Best Local Similarity 36.5%; Pred. No. 1.2e-11;
Matches 61; Conservative 29; Mismatches 63; Indels 14; Gaps 9;

QY 2 FGKLESKLSVIRNLNDVLFIDOG- NRPLFEDMTDSDCRNAPRTIFISMYKDSQP-RG 59
Db 43 FSREKTLHRLRNVSQVLVRPDLNNAFAEDVTQDEKSGSGNN-FCMCYKTKTTTSAG 101

QY 60 MAVTISVKCE-KISILSCENK-----IISFKEMNPPDNKDKSDIIFQSRVPGHDKN-M 113
Db 102 MPFASVRVEDKSYMCCEEEHGKMWVRFEGEVPKDIPG-ESNIIFFKKTFTSYSSKAF 160

QY 114 QFESSSYEGYFLACEKERDLFKLILK---EDELGDRS-TMFTVQNE 156
Db 161 KFEYSLEGRMFLAFEEEDSLRKLILKLPREDEVDETTKTTLTSHNE 207
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RESULT 11
Q918D2
ID Q918D2 PRELIMINARY; PRT; 198 AA.
AC Q918D2
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE INTERLEUKIN 18.
GN IL-18.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20508574; PubMed=11054275;
RA Schneider K., Puehler F., Baeuerle D., Elvers S., Staeheli P.,
RA Kaspers B., Weining K.C.;
RT "cDNA cloning of biologically active chicken Interleukin-18.";
RL J. Interferon Cytokine Res. 20:879-883(2000).
DR EMBL; AJ277865; CAB96214.1; -
FT CHAIN 30 198 INTERLEUKIN 18.
FT TER 198
SQ SEQUENCE 198 AA; 22918 MW; 29BB77DC3E3C6600 CRC64;

Query Match 22.4%; Score 182.5; DB 13; Length 198;
Best Local Similarity 36.8%; Pred. No. 1.2e-10;
Matches 57; Conservative 25; Mismatches 60; Indels 13; Gaps 7;

QY 13 RNLDQVLFIDOG- NRPLFEDMTDSDCRNAPRTIFISMYKDSQP-RGMATVISVKCEK 70
Db 42 RVNSQLLVVRPDLNNAFAEDVTQDEKSGS-GMYFDIHCYKTTAPSGMPVAFVSQVED 100

QY 71 ISILSCENK-----IISFKEMNPPDNKDKSDIIFQSRVPGHDKN-MQFESSSYEGYF 124
Db 101 KSYVMCCKEKHGKMWVRFEGEVPKDIPG-ESNIIFFKKTFTSCSKAFKPEYSLEQGMF 159

QY 125 LACEKERDLFKLILK---EDELGDRS-TMFTVQNE 156
Db 160 LAFEEEDSLRKLILKLPREDEVDETTKTTLTSHNE 194

RESULT 12
Q9VW71
ID Q9VW71 PRELIMINARY; PRT; 4643 AA.
AC Q9VW71
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE PUTATIVE FAT-LIKE CADHERIN PRECURSOR (CG7749 PROTEIN).
GN CG7749.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=BERKELEY;
RA MEDLINE=20196006; PubMed=107311132;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.W., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
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RESULT 13
O43031 PRELIMINARY; PRT; 381 AA.
AC O43031; Q9US93;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE HYPOTHETICAL 44.2 KDA PROTEIN C3B9.02C IN CHROMOSOME II.
GN SPBC3B9.02C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RA Wood V., Rajandream M.A., Barrell B.G., Skelton J., Churcher C.M.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 140-321 FROM N.A.
RC STRAIN=968 H90;
RA Ding B.;
RT "Generation and analysis of GFP-gene fusion library of fission
   yeast.";
CC -1- SIMILARITY: TO C.ELEGANS R11A8.2.
DR EMBL; AL022070; CAA17782.1; -.
DR EMBL; AB027944; BAA87248.1; -.
DR InterPro; IPR000467; G_patch.
DR SMART; SM00443; G_patch; 1.
KW Hypothetical protein
SQ SEQUENCE 381 AA; 44214 MW; E1542538B667549F CRC64;

Query Match 10.3%; Score 84; DB 3; Length 381;
Best Local Similarity 26.4%; Pred. No. 2.2;
Matches 39; Conservative 23; Mismatches 54; Indels 32; Gaps 7;

QY 3 GKLESKLVTRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIIISMYKDSQPRMAV 62
Db 208 GOLSSKDAF--DVNQRPTEFLGMAKPVDSLTDLIWKPKTKMF-----250
QY 63 TISVK-CEKISILSCENKIISF-KEMNPPDNKDTSDIIFFORSVPGHDKMQFESSY 120
Db 251 -LPVKPLESALNSQNEHTVEQKKSNDNL--TPSELFRRS---RDNNLSRSS--302
QY 121 EGYFLACEKERDLFKILKKEDELGDRS 148
Db 303 -----VSSKHLDYNSRNYNKRDRDPDPT 325

RESULT 14
O25249 PRELIMINARY; PRT; 452 AA.
AC O25249;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 52.7 KDA PROTEIN.
GN HP0508.
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
OX NCBI_TaxID=210;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=26695 / ATCC 700392;
RX MEDLINE=97394467; PubMed=9252185;
RA Tomb J.-F., White O., Keriavage A.R., Clayton R.A., Sutton G.G.,
RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
RA Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,

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RA Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
RA McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K.,
RA Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
RA Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E.,
RA Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
RA Venter J.C.;
RT "The complete genome sequence of the gastric pathogen Helicobacter
   pylori.";
RL Nature 388:539-547(1997).
DR EMBL; AE000565; AAD07578.1; -.
DR TIGR; HF0508; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 452 AA; 52655 MW; E2F88D85EC9EDB92 CRC64;

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Query Match 10.3%; Score 84; DB 16; Length 452;
Best Local Similarity 24.4%; Pred. No. 2.6;
Matches 41; Conservative 30; Mismatches 71; Indels 26; Gaps 8;

QY 9 LSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIIISMYKDSQPR-----58
Db 105 LVYFRQFNQOA-FLIAPNDLEYQIRATNTDINFISDDLVTFLNGFDPKIANLRKACNV 163
QY 59 -GMAVTISVKCEKISILSCEN-KIISFKEMNPPDNKDTSDIIFFORSVPGHD----NK 112
Db 164 YSVGVIIVTNTNLILSCSFEEILEKREL---DTSGVTKTSTPFSSR-VEGIDAGTLGK 219
QY 113 MQFESSYEGYF----LACEKERDLFKILKKEDELGDRSIMFTVQNE 156
Db 220 L-FSGSQSNFYAYDALVKKRKEVRIRKKREKIDSRKREIKREIKOE 266

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RESULT 15
O84500 PRELIMINARY; PRT; 866 AA.
AC O84500;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE DNA POLYMERASE I.
GN POLA OR CT493.
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DJW-37/CX;
RX MEDLINE=99000809; PubMed=9784136;
RA Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
RA Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
RA Davis R.W.;
RT "Genome sequence of an obligate intracellular pathogen of humans:
   Chlamydia trachomatis.";
RL Science 282:754-759(1998).
DR EMBL; AE001322; AAC68093.1; -.
DR HSSP; P00582; 1KFS.
DR InterPro; IPR002562; 3_5_exonuclease.
DR InterPro; IPR002421; 5_3_exonuclease.
DR InterPro; IPR002298; DNA_pol.
DR InterPro; IPR001098; DNA_pol_A.
DR InterPro; IPR000513; Exo_N_I.
DR InterPro; IPR003584; HH2.
DR Pfam; PF01367; 5_3_exonuclease; 1.
DR Pfam; PF02739; 5_3_exonuc_N; 1.
DR Pfam; PF00476; DNA_pol_A; 1.
DR PRINTS; PR00868; DNAPOLI.
DR SMART; SM00474; 35EXOC; 1.
DR SMART; SM00475; 53EXOC; 1.
DR SMART; SM00279; Hh2; 1.
DR SMART; SM00482; POLAC; 1.
KW Complete proteome.
SQ SEQUENCE 866 AA; 96583 MW; A12883E20C309D2D CRC64;

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Query Match      10.2%; Score 83.5; DB 16; Length 866;
Best Local Similarity 26.4%; Pred. No. 6.3;
Matches 34; Conservative 23; Mismatches 27; Indels 45; Gaps 8;

QY 1 YFGKLEKLSVIRNLNDQVLEFI---DOGNRPLFEDMTD-----SDCRDNAPRTIFII 49
Db 441 YFGMLASKLLAIKN---YLFVKLEEKGLKIDIFETVEQPLEAVLFAMEC-----V 486

QY 50 SNYKDSQPRGMAY---TISVKCEKIS-----ILSCENKIIISFKEMN-----PPDN 91
Db 487 GMPDLSQ--GLAVLDRDLTKLEKCSQBIYDLVGCEFNKSPKQLSDILYQRLGIEPVDK 544

QY 92 IKDTKSDII 100
Db 545 AKSTKAEVL 553

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Search completed: October 8, 2002, 10:16:41
Job time: 192 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 8, 2002, 10:05:29 ; Search time 20.63 seconds
(without alignments)
185.886 Million cell updates/sec

Title: SEQ6ILEAT73

Perfect score: 815

Sequence: 1 YFGKLESLVIRNLNDQVL.....LKKEDELGDRSMFTVQNE 157

Scoring table: BLOSUM62

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Searched: 231628 seqs, 2442594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued_Patents_AA:*
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 - 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
 - 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
 - 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
 - 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
 - 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	810	99.4	157	2	US-08-896-605A-6
2	810	99.4	157	2	US-08-896-501A-4
3	810	99.4	157	3	US-08-884-324-1
4	810	99.4	157	3	US-08-996-338-26
5	810	99.4	157	4	US-08-558-818-1
6	810	99.4	157	4	US-08-374-469A-1
7	810	99.4	157	4	US-08-832-180-1
8	810	99.4	157	4	US-08-832-198-6
9	810	99.4	193	2	US-08-896-605A-2
10	810	99.4	193	2	US-08-896-501A-2
11	810	99.4	193	4	US-08-832-180-9
12	512	62.8	157	2	US-08-502-535B-2
13	512	62.8	157	2	US-08-908-005A-2
14	512	62.8	157	3	US-08-996-338-27
15	512	62.8	157	4	US-08-558-818-7
16	512	62.8	157	4	US-08-974-469A-7
17	512	62.8	157	4	US-08-832-180-8
18	512	62.8	157	4	US-08-832-198-11
19	512	62.8	157	4	US-09-253-523-2
20	512	62.8	157	4	US-09-251-911-2
21	259	31.8	50	4	US-08-832-198-2
22	96	11.8	25	4	US-08-558-818-4
23	96	11.8	25	4	US-08-974-469A-4
24	96	11.8	25	4	US-08-832-180-4
25	96	11.8	25	4	US-08-832-198-8
26	90	11.0	17	4	US-08-832-198-5
27	83	10.2	155	6	5494663-8

Query Match 99.4%; Score 810; DB 2; Length 157;
Best Local Similarity 99.4%; Pred. No. 7.4e-88;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

US-08-896-605A-6
; Sequence 6, Application US/08896605A
; Patent No. 5879942
; GENERAL INFORMATION:
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PROCESSING ENZYME FOR POLYPEPTIDE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/896,605A
; FILING DATE: 18 July 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 207,691/1996
; FILING DATE: 19-JUL-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 156,062/1997
; FILING DATE: 30-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: TANIMOTO-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-896-605A-6

ALIGNMENTS

RESULT 1
US-08-896-605A-6
; Sequence 6, Application US/08896605A
; Patent No. 5879942
; GENERAL INFORMATION:
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PROCESSING ENZYME FOR POLYPEPTIDE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/896,605A
; FILING DATE: 18 July 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 207,691/1996
; FILING DATE: 19-JUL-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 156,062/1997
; FILING DATE: 30-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: TANIMOTO-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-896-605A-6

Patent No. 5494663
Sequence 1, Appli
Sequence 13, Appli
Sequence 20, Appli
Sequence 18, Appli
Sequence 14, Appli
Sequence 5, Appli
Sequence 184, App
Sequence 4, Appli
Sequence 11, Appli
Sequence 16, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 4, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTTIFIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTTIFIISMYKDSQPRGM 60

QY 61 AVTISVKCEKISLSCENKIISFKENPPDNKDTKSDIIFFORSVPGHDNKKMQFESSY 120
Db 61 AVTISVKCEKISLSCENKIISFKENPPDNKDTKSDIIFFORSVPGHDNKKMQFESSY 120

QY 121 EGYFLACERDLFKLILKKEDELGDRSIMFTVQNE 157
Db 121 EGYFLACERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 2
US-08-896-501A-4
; Sequence 4, Application US/08896501A
; Patent No. 5891663
; GENERAL INFORMATION:
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PROCESS FOR PRODUCING POLYPEPTIDE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 18-JUL-1997
; APPLICATION NUMBER: US/08/896,501A
; FILING DATE: 18-JUL-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 213,267/1996
; FILING DATE: 25-JUL-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 31,474/1997
; FILING DATE: 31-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: TANIMOTO=3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-896-501A-4

Query Match 99.4%; Score 810; DB 2; Length 157;
Best Local Similarity 99.4%; Pred. No. 7.4e-88;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTTIFIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTTIFIISMYKDSQPRGM 60

QY 61 AVTISVKCEKISLSCENKIISFKENPPDNKDTKSDIIFFORSVPGHDNKKMQFESSY 120
Db 61 AVTISVKCEKISLSCENKIISFKENPPDNKDTKSDIIFFORSVPGHDNKKMQFESSY 120

QY 121 EGYFLACERDLFKLILKKEDELGDRSIMFTVQNE 157
Db 121 EGYFLACERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 3
US-08-884-324-1
; Sequence 1, Application US/08884324
; Patent No. 6060283
; GENERAL INFORMATION:
; APPLICANT: Takatori OKURA
; APPLICANT: Kakuji TORIGOE
; APPLICANT: Masahi KURIMOTO
; TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE
; OF INDUCING THE PRODUCTION OF INTERFERON-
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/884,324
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 185,305/96
; FILING DATE: 27-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: OKURA=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-884-324-1

Query Match 99.4%; Score 810; DB 3; Length 157;
Best Local Similarity 99.4%; Pred. No. 7.4e-88;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTTIFIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTTIFIISMYKDSQPRGM 60

QY 61 AVTISVKCEKISLSCENKIISFKENPPDNKDTKSDIIFFORSVPGHDNKKMQFESSY 120
Db 61 AVTISVKCEKISLSCENKIISFKENPPDNKDTKSDIIFFORSVPGHDNKKMQFESSY 120

QY 121 EGYFLACERDLFKLILKKEDELGDRSIMFTVQNE 157
Db 121 EGYFLACERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 4
US-08-996-338-26
; Sequence 26, Application US/08996338
; Patent No. 6087116
; GENERAL INFORMATION:

APPLICANT: TORIGOE, Kakuji
APPLICANT: OKURA, Takanori
TITLE OF INVENTION: KURIMOTO, Masashi
TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC TO POLYPEPTIDE
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,338
FILING DATE: 22-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 74,697/1997
FILING DATE: 12-MAR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 215,488/1997
FILING DATE: 28-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 291,837/1997
FILING DATE: 09-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TORIGOE-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 157
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-996-338-26

Query Match 99.4%; Score 810; DB 3; Length 157;
Best Local Similarity 99.4%; Pred. No. 7.4e-88;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 YFGKLESLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCDNAPRTFIISMYKDSQPRGM 60
DB 1 YFGKLESLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCDNAPRTFIISMYKDSQPRGM 60
QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNKDKSDIIFQRSVPGHDNKMQFESSY 120
DB 61 AVTISVKCEKISLSCENKIISFKEMNPPDNKDKSDIIFQRSVPGHDNKMQFESSY 120
QY 121 EGYFLACEKERDLFLKILKKEDELGDRSIMFTVQNEED 157
DB 121 EGYFLACEKERDLFLKILKKEDELGDRSIMFTVQNEED 157

RESULT 5
US-08-558-818-1
Sequence 1, Application US/08558818
Patent No. 6197297
GENERAL INFORMATION:
APPLICANT: NAME: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU
APPLICANT: KENKYUJO
APPLICANT: KUNIKATA, Toshio
APPLICANT: TANIGUCHI, Mutsuko
APPLICANT: KOHNO, Keizo

APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC TO POLYPEPTIDE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W. Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect Version 5.0
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: FELICIT-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/558,818
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA: JP 58,240/95
PRIOR APPLICATION DATA: February 23, 1995
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 157 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-558-818-1
Query Match 99.4%; Score 810; DB 4; Length 157;
Best Local Similarity 99.4%; Pred. No. 7.4e-88;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 YFGKLESLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCDNAPRTFIISMYKDSQPRGM 60
DB 1 YFGKLESLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCDNAPRTFIISMYKDSQPRGM 60
QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNKDKSDIIFQRSVPGHDNKMQFESSY 120
DB 61 AVTISVKCEKISLSCENKIISFKEMNPPDNKDKSDIIFQRSVPGHDNKMQFESSY 120
QY 121 EGYFLACEKERDLFLKILKKEDELGDRSIMFTVQNEED 157
DB 121 EGYFLACEKERDLFLKILKKEDELGDRSIMFTVQNEED 157
RESULT 6
US-08-974-469A-1
Sequence 1, Application US/08974469A
Patent No. 6207641
GENERAL INFORMATION:
APPLICANT: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU
APPLICANT: KENKYUJO
APPLICANT: TORIGOE, Kakuji
APPLICANT: TANIMOTO, Tadao
APPLICANT: FUKUDA, Shigeharu
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: AGENT FOR SUSCEPTIVE DISEASE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W. Ste. 300
CITY: Washington

STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect Version 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,469A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/599,879
FILING DATE:
APPLICATION NUMBER: JP 78,357/95
FILING DATE: March 10, 1995
APPLICATION NUMBER: JP 274,988/95
FILING DATE: September 29, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TORIGOE-1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 157 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-974-469A-1

Query Match 99.4%; Score 810; DB 4; Length 157;
Best Local Similarity 99.4%; Pred. No. 7.4e-88;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 YFGKLESKLVIRNLNDQVLFIDQGNRPLFEDMTDSCRONAPRTIIFIISMYKDSQPRGM 60
Db 1 YFGKLESKLVIRNLNDQVLFIDQGNRPLFEDMTDSCRONAPRTIIFIISMYKDSQPRGM 60
QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNKDKSDIIFQFQSVPGHDKMKQFESSY 120
Db 61 AVTISVKCEKISLSCENKIISFKEMNPPDNKDKSDIIFQFQSVPGHDKMKQFESSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 7
US-08-932-180-1
Sequence 1, Application US/08832180
Patent No. 6214584
GENERAL INFORMATION:
APPLICANT: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU
APPLICANT: KENKYUJO
APPLICANT: USHIO, Shimpel
APPLICANT: TORIGOE, Kakuji
APPLICANT: TANIMOTO, Tadao
APPLICANT: OKAMURA, Haruki
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: INTERFERON- PRODUCTION INDUCING
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W. Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA

ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect Version 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/832,180
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/558,191
FILING DATE:
APPLICATION NUMBER: JP 304,203/94
FILING DATE: No. 6214584ember 15, 1994
APPLICATION NUMBER: 10048102
FILING DATE: September 18, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: USHIO-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 157 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-832-180-1

Query Match 99.4%; Score 810; DB 4; Length 157;
Best Local Similarity 99.4%; Pred. No. 7.4e-88;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 YFGKLESKLVIRNLNDQVLFIDQGNRPLFEDMTDSCRONAPRTIIFIISMYKDSQPRGM 60
Db 1 YFGKLESKLVIRNLNDQVLFIDQGNRPLFEDMTDSCRONAPRTIIFIISMYKDSQPRGM 60
QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNKDKSDIIFQFQSVPGHDKMKQFESSY 120
Db 61 AVTISVKCEKISLSCENKIISFKEMNPPDNKDKSDIIFQFQSVPGHDKMKQFESSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 8
US-08-832-198-6
Sequence 6, Application US/08832198
Patent No. 6242255
GENERAL INFORMATION:
APPLICANT: AKITA, Kenji
APPLICANT: NUKADA, Yoshiyuki
APPLICANT: FUJII, Mitsukiyo
APPLICANT: TANIMOTO, Tadao
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: PROTEIN WHICH INDUCES INTERLEUKIN-GAMMA
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM: disk
MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/832.198
; FILING DATE: 08-APR-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/721,018
; FILING DATE: 25-SEP-1996
; APPLICATION NUMBER: JP 95-270725
; FILING DATE: 26-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 96-067434
; FILING DATE: 29-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP not yet received
; FILING DATE: 20-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: AKITA-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: "Xaa" in position 73 is either
; OTHER INFORMATION: 'Ile' or 'Thr'
; US-08-832-198-6

Query Match 99.4%; Score 810; DB 4; Length 157;
Best Local Similarity 99.4%; Pred. No. 7.4e-88;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 YFGKLESLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60
Db 1 YFGKLESLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60
QY 61 AVTISVKEKISILSCENKIISFKEMNPPDNKDKTSIDIFFQRSVPGHDKMKQFESSY 120
Db 61 AVTISVKEKISILSCENKIISFKEMNPPDNKDKTSIDIFFQRSVPGHDKMKQFESSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
RESULT 9
US-08-896-605A-2
; Sequence 2, Application US/08896605A
; Patent No. 5879942
; GENERAL INFORMATION:
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PROCESSING ENZYME FOR POLYPEPTIDE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/896,501A
; FILING DATE: 18-JUL-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 213,267/1996
; FILING DATE: 25-JUL-1996

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/896,605A
; FILING DATE: 18 July 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 207,691/1996
; FILING DATE: 19-JUL-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 156,062/1997
; FILING DATE: 30-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: TANIMOTO-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 193 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-896-605A-2
Query Match 99.4%; Score 810; DB 2; Length 193;
Best Local Similarity 99.4%; Pred. No. 9.8e-88;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 YFGKLESLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60
Db 37 YFGKLESLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 96
QY 61 AVTISVKEKISILSCENKIISFKEMNPPDNKDKTSIDIFFQRSVPGHDKMKQFESSY 120
Db 97 AVTISVKEKISILSCENKIISFKEMNPPDNKDKTSIDIFFQRSVPGHDKMKQFESSY 156
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
Db 157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 193
RESULT 10
US-08-896-501A-2
; Sequence 2, Application US/08896501A
; Patent No. 5891663
; GENERAL INFORMATION:
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PROCESS FOR PRODUCING POLYPEPTIDE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/896,501A
; FILING DATE: 18-JUL-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 213,267/1996
; FILING DATE: 25-JUL-1996

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: JP 31,474/1997
;; FILING DATE: 31-JAN-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BROWDY, Roger L.
;; REGISTRATION NUMBER: 25,618
;; REFERENCE/DOCKET NUMBER: TANIMOTO=3
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-628-5197
;; TELEFAX: 202-737-3528
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 193 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-896-501A-2

Query Match 99.4%; Score 810; DB 2; Length 193;
Best Local Similarity 99.4%; Pred. No. 9.8e-88;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCDRDNAPRTIFIISMVKDSQPRGM 60
Db 37 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCDRDNAPRTIFIISMVKDSQPRGM 96

QY 61 AVTISVKCEKISLSCENKIISFKENPPDNINKDTSDIIFQFORSVPGHDKMKQFESSY 120
Db 97 AVTISVKCEKISLSCENKIISFKENPPDNINKDTSDIIFQFORSVPGHDKMKQFESSY 156

QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
Db 157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 193

RESULT 11
US-08-832-180-9
; Sequence 9, Application US/08832180
; Patent No. 6214584
; GENERAL INFORMATION:
; APPLICANT: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU
; APPLICANT: KENYUJO
; APPLICANT: USHIO, Shimpei
; APPLICANT: TORIGOE, Kakuji
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: OKAMURA, Haruki
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: INTERFERON- PRODUCTION INDUCING
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street N.W. Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect Version 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/832,180
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/558,191
; FILING DATE:
; APPLICATION NUMBER: JP 304,203/94
; FILING DATE: No. 6214584ember 15, 1994

;; APPLICATION NUMBER: 10048102
;; FILING DATE: September 18, 1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Browdy, Roger L.
;; REGISTRATION NUMBER: 25,618
;; REFERENCE/DOCKET NUMBER: USHIO=1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 628-5197
;; TELEFAX: (202) 737-3528
;; INFORMATION FOR SEQ ID NO: 9:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 193 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-832-180-9

Query Match 99.4%; Score 810; DB 4; Length 193;
Best Local Similarity 99.4%; Pred. No. 9.8e-88;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCDRDNAPRTIFIISMVKDSQPRGM 60
Db 37 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCDRDNAPRTIFIISMVKDSQPRGM 96

QY 61 AVTISVKCEKISLSCENKIISFKENPPDNINKDTSDIIFQFORSVPGHDKMKQFESSY 120
Db 97 AVTISVKCEKISLSCENKIISFKENPPDNINKDTSDIIFQFORSVPGHDKMKQFESSY 156

QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
Db 157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 193

RESULT 12
US-08-502-535B-2
; Sequence 2, Application US/08502535B
; Patent No. 5912324
; GENERAL INFORMATION:
; APPLICANT: OKAMURA, Haruki
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: TORIGOE, Kakuji
; APPLICANT: KUNIKATA, Toshio
; APPLICANT: TANIGUCHI, Mutsuko
; APPLICANT: KOHNO, Keizo
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: IFN-BETA PRODUCTION INDUCING PROTEIN AND
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/502,535B
; FILING DATE: 14-JUL-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 184162/1994
; FILING DATE: 14-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 45057/1995
; FILING DATE: 10-FEB-1995

ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: OKAMURA-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 157 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-502-535B-2

Query Match 62.8%; Score 512; DB 2; Length 157;
Best Local Similarity 64.9%; Pred. No. 9.1e-53;
Matches 100; Conservative 26; Mismatches 26; Indels 2; Gaps 2;
QY 2 FGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIIISMVKDSQPRGMA 61
DB 2 FGLRCHTTAVIRINNDQVLFVDK-RQPVFEDMTDIDQSASEPQTRLIIYMYKDSEVRGLA 60
QY 62 VTISVKCKISILSCENKIISKEMNPPDNKDKTSIDIFFORSVPGHDKNMQFESSSYE 121
DB 61 VTLVKDKSKXSTLSCKNKIISPEEMDPENIDDIQSDLIFFQKRVPGH-NKMEFESSLYE 119
QY 122 GYFLACEKERDLFKLILKKEDELGDRSIMFTVON 155
DB 120 GHFLACQKEDDAFLKILKDKDENGKDSVMFTLTN 153

RESULT 13

US-08-908-005A-2
Sequence 2, Application US/08908005A
Patent No. 5914253
GENERAL INFORMATION:
APPLICANT: OKAMURA, Haruki
APPLICANT: TANIMOTO, Tadao
APPLICANT: TORIGOE, Kakuji
APPLICANT: KUNIKATA, Toshio
APPLICANT: TANIGUCHI, Mutsuko
APPLICANT: KOHNO, Keizo
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: IFN-BETA PRODUCTION INDUCING PROTEIN AND
TITLE OF INVENTION: MONOCLONAL ANTIBODY OF THE SAME
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 11-AUG-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/502,535
FILING DATE: 14-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 184162/1994
FILING DATE: 14-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 45057/1995
FILING DATE: 10-FEB-1995

ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: OKAMURA-2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 157 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-908-005A-2

Query Match 62.8%; Score 512; DB 2; Length 157;
Best Local Similarity 64.9%; Pred. No. 9.1e-53;
Matches 100; Conservative 26; Mismatches 26; Indels 2; Gaps 2;
QY 2 FGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIIISMVKDSQPRGMA 61
DB 2 FGLRCHTTAVIRINNDQVLFVDK-RQPVFEDMTDIDQSASEPQTRLIIYMYKDSEVRGLA 60
QY 62 VTISVKCKISILSCENKIISKEMNPPDNKDKTSIDIFFORSVPGHDKNMQFESSSYE 121
DB 61 VTLVKDKSKXSTLSCKNKIISPEEMDPENIDDIQSDLIFFQKRVPGH-NKMEFESSLYE 119
QY 122 GYFLACEKERDLFKLILKKEDELGDRSIMFTVON 155
DB 120 GHFLACQKEDDAFLKILKDKDENGKDSVMFTLTN 153

RESULT 14

US-08-996-338-27
Sequence 27, Application US/08996338
Patent No. 6087116
GENERAL INFORMATION:
APPLICANT: TORIGOE, Kakuji
APPLICANT: OKURA, Takanori
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: POLYPEPTIDES
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 22-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 74,697/1997
FILING DATE: 12-MAR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 215,488/1997
FILING DATE: 28-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 291,837/1997
FILING DATE: 09-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TORIGOE-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 157
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-996-338-27

Query Match 62.8%; Score 512; DB 3; Length 157;
Best Local Similarity 64.9%; Pred. No. 9.1e-53;
Matches 100; Conservative 26; Mismatches 26; Indels 2; Gaps 2;
QY 2 FGKLESKLVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIIISMYKDSQPRGMA 61
Db 2 FGRHCTTAVIRNLNDQVLFVDK-RQPVFEDMTDIDQASAPQTRLIIYMYKDSQPRGMA 60
QY 62 VTISVKCEKISILSCENKIIISFKEMNPPDNIKDTKSDIIFFQSVPGHDKNMQFESSSYYE 121
Db 61 VTLVKDSKXSTLSCKNKKIISFEEMDPDENIDQSLIFFQKRVPGH-NKMEFESSLYE 119
QY 122 GYFLACEKERDLFKLILKKEDELGDRSIMFTVQN 155
Db 120 GHFLACQKEDDAFKLILKKEDELGDRSIMFTLTN 153

RESULT 15

US-08-558-818-7
Sequence 7, Application US/08558818
Patent No. 6197297
GENERAL INFORMATION:
APPLICANT: NAME: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU
APPLICANT: KENKYUJO
APPLICANT: KUNIKATA, Toshio
APPLICANT: TANIGUCHI, Mutsuko
APPLICANT: KOHNO, Keizo
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC TO POLYPEPTIDE
TITLE OF INVENTION: WHICH INDUCES INTERFERON- PRODUCTION
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W. Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect Version 5.0
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: FELICI-1
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/558,818
FILING DATE:

CLASSIFICATION: 530
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: JP 58,240/95
PRIOR APPLICATION DATA: February 23, 1995
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 157 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: mouse
INDIVIDUAL ISOLATE: liver
US-08-558-818-7
Query Match 62.8%; Score 512; DB 4; Length 157;
Best Local Similarity 64.9%; Pred. No. 9.1e-53;
Matches 100; Conservative 26; Mismatches 26; Indels 2; Gaps 2;
QY 2 FGKLESKLVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIIISMYKDSQPRGMA 61
Db 2 FGRHCTTAVIRNLNDQVLFVDK-RQPVFEDMTDIDQASAPQTRLIIYMYKDSQPRGMA 60
QY 62 VTISVKCEKISILSCENKIIISFKEMNPPDNIKDTKSDIIFFQSVPGHDKNMQFESSSYYE 121
Db 61 VTLVKDSKXSTLSCKNKKIISFEEMDPDENIDQSLIFFQKRVPGH-NKMEFESSLYE 119
QY 122 GYFLACEKERDLFKLILKKEDELGDRSIMFTVQN 155
Db 120 GHFLACQKEDDAFKLILKKEDELGDRSIMFTLTN 153

Search completed: October 8, 2002, 10:14:17
Job time: 528 sec

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